

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: June 7, 2003, 19:50:27 ; Search time 2978 Seconds
(without alignments)
11150.538 Million cell updates/sec

Title: US-09-617-174c-1
Perfect score: 1141
Sequence: 1 agataagcacagcagagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sta.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vt.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_ox.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sta.*
- 28: em_un.*
- 29: em_vt.*
- 30: em_hcg_hum.*
- 31: em_hcg_inv.*
- 32: em_hcg_other.*
- 33: em_hcg_mus.*
- 34: em_hcg_pln.*
- 35: em_hcg_rod.*
- 36: em_hcg_man.*
- 37: em_hcg_vrt.*
- 38: em_sy.*
- 39: em_hngo_hum.*
- 40: em_hngo_mus.*
- 41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1129.8	99.0	170269	9	AC090307	AC090307 Homo sapi
C	1129.8	99.0	173252	9	AC036176	AC036176 Homo sapi
C	1129.8	99.0	173836	2	AP001404	AP001404 Homo sapi
C	745.4	65.3	12426	6	AX251236	AX251236 Sequence
C	723.4	63.4	12426	6	AX251235	AX251235 Sequence
C	612	53.6	214212	2	AC015793	AC015793 Homo sapi
C	437.6	38.4	214212	2	AC015793	AC015793 Homo sapi
C	203.4	17.8	44255	9	AL356309	AL356309 Human DNA
C	199.4	17.5	84577	9	AC079927	AC079927 Homo sapi
C	196.6	17.2	143721	9	AC117414	AC117414 Homo sapi
C	195	17.1	2343	9	AK023951	AK023951 Homo sapi
C	195	17.1	71872	9	AL133390	AL133390 Human DNA
C	195	17.1	147259	2	AC019248	AC019248 Homo sapi
C	195	17.1	184703	9	AL365215	AL365215 Human DNA
C	194	17.0	164167	2	AC090104	AC090104 Homo sapi
C	194	17.0	189018	9	AC091185	AC091185 Homo sapi
C	193.4	17.0	158806	2	AL591132	AL591132 Homo sapi
C	193.4	17.0	168834	2	AL355583	AL355583 Homo sapi
C	193.4	17.0	197864	9	HSY214810	AL022344 Human DNA
C	193.4	17.0	200882	2	AL591181	AL591181 Homo sapi
C	193.4	17.0	214180	2	AL360082	AL360082 Homo sapi
C	193.4	17.0	238379	2	AL590986	AL590986 Homo sapi
C	193.4	17.0	300000	17	AL645813	AL645813 Human DNA
C	192.8	16.9	204037	2	AC016813	AC016813 Homo sapi
C	192.8	16.9	165152	9	AC012308	AC012308 Homo sapi
C	192.6	16.9	196533	9	CNS000V1	AL056870 Homo sapi
C	191.6	16.8	148555	2	AP004711	AP004711 Homo sapi
C	191.6	16.8	15614	2	AC012620	AC012620 Homo sapi
C	191.6	16.8	160883	9	AC021498	AC021498 Homo sapi
C	191.6	16.8	191063	9	AC091825	AC091825 Homo sapi
C	191.4	16.8	162554	9	AC079354	AC079354 Homo sapi
C	190.8	16.7	67197	9	AF510423S1	AF510423 Homo sapi
C	190.8	16.7	100007	9	AC099397	AC099397 Homo sapi
C	190.8	16.7	102837	9	HS22202	295329 Human DNA s
C	190.6	16.7	198779	2	AC024619	AC024619 Homo sapi
C	190.4	16.7	109902	9	HSJ46C2	AL132775 Human DNA
C	190.4	16.7	146578	9	AC012468	AC012468 Homo sapi
C	190.2	16.7	150477	2	AC024441	AC024441 Homo sapi
C	190.2	16.7	159265	2	AL157942	AL157942 Homo sapi
C	190.2	16.7	168759	2	AC068307	AC068307 Homo sapi
C	190.2	16.7	168835	2	AC126308	AC126308 Homo sapi
C	190.2	16.7	203726	9	AC084871	AC084871 Homo sapi
C	190	16.7	110000	2	AL357131_1	Continuation (2 of
C	190	16.7	139325	9	AL589943	AL589943 Human DNA
C	190	16.7	161695	2	AC079849	AC079849 Homo sapi

ALIGNMENTS

RESULT 1
AC090307
LOCUS AC090307 170269 bp DNA linear PRI 30-DEC-2001
DEFINITION Homo sapiens chromosome 18, clone RP11-851B10, complete sequence.
ACCESSION AC090307
VERSION AC090307.7 GI:16041402
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 170269)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-851B10
JOURNAL Unpublished

repeat region

repeat_region	17377..17572 /rpt family="MIR3" complement(20036) .20330) /rpt family="Charlie1" complement(20333..20486) /rpt family="Charlie1" 20625..20691 /rpt family="L2" complement(20829..21075) /rpt family="MLT1C" complement(21104..21336) /rpt family="MLT1C" complement(22112..22391) /rpt family="AluSx" 22506..22581 /rpt family="Tigger5" complement(23483..23664) /rpt family="MIR" 23979..24190 /rpt family="MER20" complement(25404..25455) /rpt family="MER5B" complement(25769..25853) /rpt family="AluS" 25964..25998 /notes="Single clone coverage" 25999..26004 /notes"<30 qual single clone coverage" 26005..26009 /notes="Single clone coverage" complement(26204..26297) /rpt family="MER5A" 27103..27222 /rpt family="MIR3" 27281..27573 /rpt family="AluY" 28033..28160 /rpt family="MIR" complement(28205..28490) /rpt family="LIPB2" 28491..28801
Query Match	99.0%; Score 1129.8; DB-9; Length 170269;
Best Local Similarity	99.4%; Pred. No. 4.5e-308;
Matches 1134; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
Qy	1 AGATAGCACAGACAGAGAACCAAGCTCCGTTTCAGGTCTCTTCTCGAGGCTGATTGG 60
Db	13276 AGATAGCACAGACAGAGAACCAAGCTCCGTTTCAGGTCTCTTCTCGAGGCTGATTGG 13335
Qy	61 GCTGGAAGGGAGTAGCTCCACCAAATGAAGAAGCTGTGGGAAGACAGGAGGACAAGAAC 120
Db	13336 GCTGGAAGGGAGTAGCTCCGCCAAATGAAGAAGCTGTGGGAAGACAGGAGGACAAGAAC 13395
Qy	121 AGGCTCCAAGACAGATTTCAGACAGAGCTCGGTACTCTTTTTTCTTTTGTTTCTTTT 180
Db	13396 AGGCTCCAAGACAGATTTCAGACAGAGCTCGGTACTCTTTTTTCTTTTGTTTCTTTT 13455
Qy	181 GCTCTGTCAACCCAGGCTGAAGTAGTACGTGTTAGTCTCAGGGCTCAGTGCAGCTTGAACCTC 240
Db	13456 GCTCTGTCAACCCAGGCTGAAGTAGTACGTGTTAGTCTCAGGGCTCAGTGCAGCTTGAACCTC 13515
Qy	241 CCAGGCTCAAGTTCATCTCTCGTCTCAGCTTTTCCAAGTAATCGGGACACACAGGCAATGCAT 300
Db	13516 CCAGGCTCAAGTTCATCTCTCGTCTCAGCTTTTCCAAGTAATCGGGACACACAGGCAATGCAT 13575
Qy	301 CACCACGCTAGGCTATTGTTTATCATTTTTTGTAGAGATGGGGTCTCACCATGTTGCCCA 360
Db	13576 CACCACGCTAGGCTATTGTTTATCATTTTTTGTAGAGATGGGGTCTCACCATGTTGCCCA 13635
Qy	361 GGTTGGTCTCAAACTCCTGGGCTCAAGCAATCGGTCAAGTCAACTCCCCAAATGCTGG 420
Db	13636 GGTTGGTCTCAAACTCCTGGGCTCAAGCAATCGGTCAAGTCAACTCCCCAAATGCTGG 13695

Tue Jun 10 08:56:17 2003

On Mar 19, 2002 this sequence version replaced gi:17647019.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9215

Center clone name: 635_N_19

FEATURES

source

1. 173252

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="18"

/map="18"

/clone="RP11-635N19"

/clone_lib="RPC1-11 Human Male BAC"

2. 295

/rpt_family="MER65A-int"

296. 330

/rpt_family="(TTTA)n"

331. 475

/rpt_family="MER65A-int"

complement(553. 904)

/rpt_family="THE1B"

1274. 1618

/rpt_family="MER65A-int"

1619. 1955

/rpt_family="MER7A"

1956. 2254

/rpt_family="MER65A-int"

2255. 2403

/rpt_family="FRAM"

2404. 3470

/rpt_family="MER65A-int"

3557. 3674

/rpt_family="MER65A-int"

3675. 3991

/rpt_family="AluX"

3992. 4132

/rpt_family="MER65A-int"

4133. 4439

/rpt_family="AluX"

4440. 4676

/rpt_family="MER65A-int"

4775. 4826

/rpt_family="MER65A-int"

4909. 5110

/rpt_family="MER65A-int"

5195. 6555

/rpt_family="MER65A-int"

6557. 7121

/rpt_family="MER65A-int"

7124. 7442

/rpt_family="MER65A-int"

7443. 7892

/rpt_family="MER65A"

8797. 8975

/rpt_family="MER5A"

9249. 9351

/rpt_family="MIR"

9719. 9880

/rpt_family="LIMB1"

complement(10160. 10263)

/rpt_family="MIR3"

10453. 10523

/rpt_family="MER94"

complement(10639. 10937)

/rpt_family="AluX"

COMMENT

Campiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173252)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (19-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 173252)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gird, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenka, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE
JOURNALREFERENCE
AUTHORSTITLE
JOURNALREFERENCE
AUTHORSTITLE
JOURNAL

1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555, Japan
 E-mail: hattori@gsf.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-42-778-9923, Fax: 81-42-778-9924
 On Jul 14, 2000 this sequence version replaced gi:18117315.
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsf.riken.go.jp
 ----- Project Information
 Center project name: HumDraft18
 Center clone name: RP11-851B10
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 171265 bases at least Q40
 Consensus quality: 172100 bases at least Q30
 Consensus quality: 172469 bases at least Q20
 Insert size: 172836; sum-of-contigs
 Quality coverage: 10.50x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 68896 contig of 68896 bp in length
 68997 95899 contig of 26903 bp in length
 96000 119268 contig of 23269 bp in length
 119369 141739 contig of 22371 bp in length
 141840 152655 contig of 10816 bp in length
 152756 159466 contig of 6711 bp in length
 159567 163465 contig of 3899 bp in length
 163566 166433 contig of 2868 bp in length
 166534 170112 contig of 3579 bp in length
 170213 172095 contig of 1883 bp in length
 172196 173836 contig of 1641 bp in length.

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 68896: contig of 68896 bp in length
 68897 68996: gap of 100 bp
 68997 95899: contig of 26903 bp in length
 95900 95999: gap of 100 bp
 96000 119268: contig of 23269 bp in length
 119269 119368: gap of 100 bp
 119369 141739: contig of 22371 bp in length
 141740 141839: gap of 100 bp
 141840 152655: contig of 10816 bp in length
 152656 152755: gap of 100 bp
 152756 159466: contig of 6711 bp in length
 159467 159566: gap of 100 bp
 159567 163465: contig of 3899 bp in length
 163466 163565: gap of 100 bp
 163566 166433: contig of 2868 bp in length
 166434 166533: gap of 100 bp
 166534 170112: contig of 3579 bp in length
 170113 170212: gap of 100 bp
 170213 172095: contig of 1883 bp in length
 172096 172195: gap of 100 bp
 172196 173836: contig of 1641 bp in length.

Location/Qualifiers
 1. .173836
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

FEATURES
 source

/chromosome="18"
 /map="18q22"
 /clone="RP11-851B10"
 1. .68896
 /note="assembly_fragment"
 68997. .95899
 /note="assembly_fragment clone_end:T7 vector_side:right"
 96000. .119268
 /note="assembly_fragment"
 119369. .141739
 /note="assembly_fragment"
 141840. .152655
 /note="assembly_fragment"
 152756. .159466
 /note="assembly_fragment"
 159567. .163465
 /note="assembly_fragment"
 163566. .166433
 /note="assembly_fragment clone_end:SP6 vector_side:left"
 166534. .170112
 /note="assembly_fragment"
 170213. .172095
 /note="assembly_fragment"
 172196. .173836
 /note="assembly_fragment"
 BASE COUNT 53047 a 34410 c 33807 g 51570 t 1002 others
 ORIGIN

Query Match 99.0%; Score 1129.8; DB 2; Length 173836;
 Best Local Similarity 99.4%; Pred. No. 4.5e-308; Indels 0; Gaps 0;
 Matches 1134; Conservative 0; Mismatches 7;
 QY 1 AGATAAGCACAGCAGAGAGCAACAGCTCCGTTTCAGGTCCTTTCTCTGAGGCTGATTTCG 60
 Db 150724 AGATAAGCACAGCAGAGAGCAACAGCTCCGTTTCAGGTCCTTTCTCTGAGGCTGATTTCG 150665
 QY 61 GCTGGAAGGGAGTAGTCCCAATGAAGAGCTGTGGAGAGCAGGAGCAAGAAC 120
 Db 150664 GCTGGAAGGGAGTAGTCCCAATGAAGAGCTGTGGAGAGCAGGAGCAAGAAC 150605
 QY 121 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGCGTACTCTCTTTTCTTTTCTTTTCTTTT 180
 Db 150604 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGCGTACTCTCTTTTCTTTTCTTTTCTTTT 150545
 QY 181 GCTCTGTCAACCAGGCTGAAGTACAGTGTGTAGCTCAGGCTCAGGCTCAGGCTTTCACCTC 240
 Db 150544 GCTCTGTCAACCAGGCTGAAGTACAGTGTGTAGCTCAGGCTCAGGCTTTCACCTC 150485
 QY 241 CCAGGCTCAAGTATCT 300
 Db 150484 CCAGGCTCAAGTATCT 150425
 QY 301 CACACAGCTAGGCTATTGTTTTCATATTTTGTAGAGATGGGGTCTCACCTGTTGCCCA 360
 Db 150424 CACACAGCTAGGCTATTGTTTTCATATTTTGTAGAGATGGGGTCTCACCTGTTGCCCA 150365
 QY 361 GGTGTGTCAAACTCTCTGGGCTCAAGCAATCGGCTCAGTCAACTCCCAAACTCTCTG 420
 Db 150364 GGTGTGTCTCAAACTCTCTGGGCTCAAGCAATCGGCTCAGTCAACTCCCAAACTCTCTG 150305
 QY 421 GATTACAGGCGTCAAGCCAGGCGCCAGGCGTGAATCTCTATCAAGGATTTTAAAAA 480
 Db 150304 GATTACAGGCGTCAAGCCAGGCGCCAGGCGTGAATCTCTATCAAGGATTTTAAAAA 150245
 QY 481 GAAACTTCTCGCCCAACCAATTAACAATATCTCTTACCAATTTGGTAGTAATATTTCG 540
 Db 150244 GAAACTTCTCGCCCAACCAATTAACAATATCTCTTACCAATTTGGTAGTAATATTTCG 150185
 QY 541 CTAATAGTACTTAATTTTGTAGGACGCTGTTTATATATATATATATATATATATATATATAT 600
 Db 150184 CTAATAGTACTTAATTTTGTAGGACGCTGTTTATATATATATATATATATATATATATATAT 150125
 QY 601 TTGATTGCTTTCTTGTTTAAATGGGCGAGCTACCTCTCTTGGCATCTTAGCAAGATGAGCTGC 660

Db	150124	TTGATTTGCTTTCTGTTTAAATGGGAGCTACTCTCTTTGGCATCTTAGCAGATGAGCTGC	150065	
Qy	661	TGCAGTTTACACAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCGCCACCAACGTGCTCGAG	720	
Db	150064	TGCAGTTTACACAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCGCCACCAACGTGCTCGAG	150005	
Qy	721	AAATTTGTAGTGTACTATCATCACACATTAATTTATTTTCATCGAATATTTTCACCTTCC	780	
Db	150004	AAATTTGTAGTGTACTATCATCACACATTAATTTATTTTCATCGAATATTTTCACCTTCC	149945	
Qy	781	GGTCTCGGTGGGCCGAGAGGATGCGGTACGCATGTCTGTACGTATGATGATTAAGTCACTCAC	840	
Db	149944	GGTCTCGGTGGGCCGAGAGGATGCGGTACGCATGTCTGTACGTATGATGATTAAGTCACTCAC	149885	
Qy	841	AGCCCTTCTCTGCCGCAACATGTTTGGAGGCTTTTGGAAAGCTGTGCAGACAAACCAACT	900	
Db	149884	AGCCCTTCTCTGCCGCAACATGTTTGGAGGCTTTTGGAAAGCTGTGCAGACAAACCAACT	149825	
Qy	901	TCAGCTGAATCATCTCTTTTCAATTGTGCAAGCTGCCAAGAGCTTTGAGTGGAGAGG	960	
Db	149824	TCAGCTGAATCATCTCTTTTCAATTGTGCAAGCTGCCAAGAGCTTTGAGTGGAGAGG	149765	
Qy	961	AGTGCCGCGAGGCGGGGCGGG	1020	
Db	149764	AGTGCCGCGAGGCGGGGCGGG	149705	
Qy	1021	GCTGCCAGGTGAGCCAGCGTGTCTTGCTGCCAGACAGCTGCGCTCCACATCCAGGTCT	1080	
Db	149704	GCTGCCAGGTGAGCCAGCGTGTCTTGCTGCCAGACAGCTGCGCTCCACATCCAGGTCT	149645	
Qy	1081	TTGTGCTCTCGCTTGGCTTTCCTTTTCCAGCGATTTTCCAGGATAACTGTGACTCCAG	1140	
Db	149644	TTGTGCTCTCGCTTGGCTTTCCTTTTCCAGCGATTTTCCAGGATAACTGTGACTCCAG	149585	
Qy	1141	G 1141		
Db	149584	G 149584		
RESULT 4				
AX251236/c				
LOCUS	AX251236	12426 bp	DNA	linear
DEFINITION	Sequence 204 from Patent WO0168912.			
ACCESSION	AX251236			
VERSION	AX251236.1 GI:15984659			
KEYWORDS	synthetic construct.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 12426)			
AUTHORS	Olek, A., Piepenbrock, C. and Berlin, K.			
TITLE	Diagnosis of diseases associated with tumor suppressor genes and			
JOURNAL	oncogenes			
PATENT	Patent: WO 0168912-A 204 20-SEP-2001;			
EPIDEMIOLOGY	Epigenomics AG (DE)			
FEATURES	Location/Qualifiers			
source	1..12426			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			
	/note="chemically treated genomic DNA (Homo sapiens)"			
BASE COUNT	3791 a	137 c	2517 g	5981 t
ORIGIN				
Query Match 65.3%; Score 745.4; DB 6; Length 12426;				
Best Local Similarity 78.4%; Pred. No. 1.4e-199;				
Matches 893; Conservative 0; Mismatches 246; Indels 0; Gaps 0;				
Qy	1	AGATAAGCAGCAGAGAGCAACCGCTCCGTTTCAGGTCCTTTCCCTGAGGCTGATTCG	60	
Db	8506	AAATAAACACACAAAAAACAAACCAACTCCGTTTCAATCTCTTCCCTTAAATCTAATTCG	8447	
Qy	61	GCTGGAAGGAGTAGTGGTCCCAACCAATGAAGAAGCTGTGGGAAGACAGGAGGACAGAAC	120	

Db	8446	ACTAAAAAATAATATCCCGCAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	8387	
Qy	121	AGGCTCCAGAGAGATTTTCAGAGCAGAGCTCGTACTCTCTTTCTTTTCTTTTCTTTTCTTTT	180	
Db	8386	AAATCCACGAAAAAATTTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA	8327	
Qy	181	GCTGTCTCACCAGGCTGAAGTACAGTGGTGTAGCTCAGCGCTCAGCTGAGCTGACCTTGGACCTC	240	
Db	8326	ACTCTATCACCACCAACTAAATACATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	8267	
Qy	241	CAGGCTCAAGTGATCTCTCTCTCAGCTTTTCCAAAGTAATCTGGAACCAACAGGAGTATGAT	300	
Db	8266	CCAAAACTCAATAATCTCTCTCTCAACTTTTCCAAATAATTAATTAATTAATTAATTAATTAAT	8207	
Qy	301	CACCACTGAGCTATGTTTGTAGAGATGGGCTCTCACCATCTGTCGCCCA	360	
Db	8206	CACCACTGAGCTATGTTTGTAGAGATGGGCTCTCACCATCTGTCGCCCA	8147	
Qy	361	GGTGTGTCTCAAACTCTCGGCTCAAGCAATCGCTCAGCTCAACCTCCCAATGCTGG	420	
Db	8146	AATTAATCTCAAACTCTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAACTCAAA	8087	
Qy	421	GATTACAGGCTGAGCCAGCGGCTGAGTAACTCTTAATCAAGATTTTAAAAA	480	
Db	8086	AATTAACAAACGTAACCTCAACGCGGCAAACTTAATAATCTTAATCAAAAAATTTAAAAA	8027	
Qy	481	GAACTTCTCGGCCCAACCAATATCTCTTACCCTTGGTGGTAAATATTTT	540	
Db	8026	AAAACTTCTAGCGCAACCAATATCTCTTACCCTTGGTGGTAAATATTTT	7967	
Qy	541	CTAATAGTACCTAAATTTTAGGTAGGCTGTTTATACATATATCCATCTCTCTTTT	600	
Db	7966	CTAATAGTACCTAAATTTTAGGTAGGCTGTTTATACATATATCCATCTCTCTTTT	7907	
Qy	601	TTGATTTCTTTCTGTTTAAATGGGAGTACCTCTCTTGGCATCTAGCAGATGAGCTGC	660	
Db	7906	TTAAATTTCTTTCTAATTAATAAACTACCTCTCTTAACTCTTAACTCTTAACTCTTAACTCT	7847	
Qy	661	TGCAGTTTACAAAAAGATGAGATCAGAGTACTTTTGTGCGCAACAGCTGCTGAG	720	
Db	7846	TACAATTTACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	7787	
Qy	721	AAATTTGATGTTACTATCATCACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT	780	
Db	7786	AAATTTATATATTTACTATCATCACACATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT	7727	
Qy	781	GCTCTGCTGGGCGGAGAGGATGCGGTACGATGCTCTGTAGTATGATGATGATGATGATGATGATG	840	
Db	7726	GATCTTACGTAAACCGAAAAAATAACCGTACGCATATCTATACGTATACATATACTAC	7667	
Qy	841	AGCCCTTCTCTCGCCGACATGTTGGAGGCTTTTGGAGCTCTGAGACCAACAGCAACT	900	
Db	7666	AACCCCTTCTTACCGGACATATTAATAAACCTTTTAAAAAATAAATAAATAAATAAATAAATAA	7607	
Qy	901	TCAGCTGAATCATCTCTTTCAATTTGTGCAAGCTGCCAAGAGCTTGAAGTGGAGAGG	960	
Db	7606	TCACCTTAATCATTTCTTTCAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	7547	
Qy	961	AGTGGCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1020	
Db	7546	AATACCGCGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACGAAACG	7487	
Qy	1021	GCTGCCAGGTGAGCCACCGCTCTCTGCCAGACAGCGTGGCTGCCATCCAGCTCT	1080	
Db	7486	ACTACCCCAATAAACCCCGCTACTTCTACCCCAACAGCATCGCTCTCCCAATCT	7427	
Qy	1081	TTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1139	
Db	7426	TTATACTCTCTGCTTACCTATTCTTTTCCAGCATTTTCCAAAAATTAATTAATTAATTAATTAAT	7368	

Db	4581	TGTTAGTTTATATAAAGAAATCGAGATTAGAGTAATTTTTTGTGTTATTAACTGTTTGAG	4640
Qy	721	AAATTTGTAGTTACTATCATCACACATTACTTTTATTTTATTCATCGAATATTTTCACTTCC	780
Db	4641	AAATTTGTAGTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTT	4700
Qy	781	GGTCTCGTGGCGGCGAGAGGATTGCGTACGATCTGTAGTATGATGTAATCTAC	840
Db	4701	GGTTTGGTGGTCCGAGAGGATTGCGTACGATCTGTAGTATGATGTAATCTAC	4760
Qy	841	AGCCCTCTCTGCGGCGAATGTTGAGGCTTTTGGAGCTGTGCGAGACACAGCAACT	900
Db	4761	AGTTTTTTTTTGTTCGAATATGTTGAGGTTTTTGGAGGTTTTTGGAGGTTTTGATGTAAT	4820
Qy	901	TCAGCTCAATCATCTCTTTCAATTTGGAACAAGCTGCCAAGAGGCTTGTAGTAGGAGG	960
Db	4821	TTAGTTTGAATTTATTTTTTTTAAATTTGGAATAGTTGTTTAAAGGTTTGGTAGGAGG	4880
Qy	961	AGTCCGCGAGGCGGGCGGGCGGTGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	1020
Db	4881	AGTCTCGTCCGAGGCGGGCGGGCGGTGAGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	4940
Qy	1021	GCTGCCAGGTGAGCCACCGCTCTCTGCCAGACACGCTCCCTCCATCCAGCTCT	1080
Db	4941	GTTGTTTGGTGGATTTATCGTTGTTTGTGTTTATGATACGGTCGTTTTTATTTAGGTT	5000
Qy	1081	TTGTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140
Db	5001	TTGTTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	5060
Qy	1141	G 1141	
Db	5061	G 5061	

AX251235	AX251235	12426 bp	DNA	linear	PAT 05-OCT-2001
LOCUS	Sequence 203 from Patent WO0168912.				
DEFINITION	Sequence 203 from Patent WO0168912.				
ACCESSION	AX251235				
VERSION	AX251235.1	GI:15984658			
KEYWORDS	synthetic construct.				
SOURCE	artificial construct.				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 12426)				
AUTHORS	Olek.A., Piepenbrock.C. and Berlin.K.				
TITLE	Diagnosis of diseases associated with tumor suppressor genes and				
JOURNAL	oncogenes				
Patent:	WO 0168912-A 203 20-SEP-2001;				
Epigenomics AG (DE)					
FEATURES	Location/Qualifiers				
source	1..12426				
BASE COUNT	3527 a	137 c	2591 g	6171 t	
ORIGIN					
Query Match	63.4%; Score 723.4; DB 6; Length 12426;				
Best Local Similarity	77.1%; Pred. No. 2.4e-193;				
Matches	880; Conservative 0; Mismatches 261; Indels 0; Gaps 0;				
Qy	1	AGATAGCAGCAGAGAGACCAACGAGCTCCGTTTCAGGTCCTTTCTGTAGGCTGATTCG	60		
Db	3921	AGATAAGTATAGTAGAGAGTAATAGTTTCGTTTGTAGTTTTCGTTTGTAGATTGATTCG	3980		
Qy	61	GCTGGAAGGAGTAGTCCCAACCAATGAAGAAGCTGTGGGAAGACAGGAGGACAGAAC	120		
Db	3981	GTTGGAAGGAGTAGGTTTCGTTTAAATGAAGAAGTTGTGGGAAGATAGGAGGATAAGAT	4040		
Qy	121	AGGCTCCAGAGAGATTTCAGAGCAGAGCTGGTACTCCTTTTTTCTTTTTTGTTCCTTTT	180		
Db	4041	AGGTTTTACGAAGAGATTTTGTAGAGTAGAGTTGCGTATTTTTTTTTTTTTTTTTTTTT	4100		
Qy	181	GCTCTGTCAACGAGCTGAAGTAGTACAGTGTGTTAGTCTCACGGCTCACTGAGCTTTGACCTC	240		
Db	4101	GTTTGTGTTTATTTAGGTTGAAGTATAGTTGGTTAGTTTACGGTTTATTTAGTTTGTATTT	4160		
Qy	241	CCAGGCTCAAGTATCTCTGCTCAGCTTTCAGTAAGTAACTGGGACACAGGATCAT	300		
Db	4161	TTAGGTTTAAAGTATTTTTCGTTTGTAGTTTAAAGTAATTTGGGATTAAGGATGATAT	4220		
Qy	301	CACCAAGCTAGGCTATTTGTTTACATTTTTTGTAGAGATGGGCTCTCACCATGTTGCCCA	360		
Db	4221	TATTATATTTAGGTTATTTGTTTATTTTTTGTAGAGATGGGTTTATTTATGTTGTTTA	4280		
Qy	361	GGTTCGTCTCAAACTCTCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAATGCTGG	420		
Db	4281	GGTTGGTTTAAATTTTTTGGGTTTAAAGTAATTCGTTTACGTTAAATTTTTTAAATGTTGG	4340		
Qy	421	GATTACAGGCTGAGCCACCGGCGGAGGCTGAGTAATCTTAATCAAGGATTTTAAAAA	480		
Db	4341	GATTATAGGCTGAGTATTCGCGTTTGGGTTTAAAGTAATTTTAAATATAGGATTTTAAAAA	4400		
Qy	481	GAAACTTCTGCGCGCACCCCAATTAACAATATCTCTACCAATTTGGTAGTAAATATTTTG	540		
Db	4401	GAAATTTTGGGTTATTTATTAATAATATTTTTTAAATTTGGTAGTAAATATTTTG	4460		
Qy	541	CTAATAGTACCTAAATTTTGTAGTAGGCACTGGTTTATACATATATCCATTCCTCTTTT	600		
Db	4461	TTAATAGTATTTAAATTTTGTAGTAGGATTTGTTTATATATATATTTTTTTTTTTTTT	4520		
Qy	601	TTGATTTCTTCTGTTTAAATGAGGAGCTACCTCTCTTGGCATCTAGCAGAAATGAGCTGC	660		
Db	4521	TTGATTTCTTCTGTTTAAATGAGGAGCTACCTCTCTTGGCATCTAGCAGAAATGAGCTGC	4580		
Qy	661	TGCAGTTTACAAAAAGAAATGGAGATCAGAGTACTTTTGTGCCACCAACGCTGCTGAG	720		

AC015793 214212 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 18 clone RP11-1117D15 map 18, LOW-PASS
SEQUENCE SAMPLING.
AC015793
AC015793.2 GI:7144769
HTG; HTGS_PHASE0.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214212)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-1117D15
Unpublished
2 (bases 1 to 214212)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barina,N., Beckerly,R., Boguslavsky,L., Boukhgaiter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArillano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teafaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:6446894.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1590
 Center clone name: L117_D_15

* NOTE: This record contains 240 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1 695: contig of 695 bp in length
 * 696 795: gap of 100 bp
 * 796 1513: contig of 718 bp in length
 * 1514 1613: gap of 100 bp
 * 1614 2337: contig of 724 bp in length
 * 2338 2437: gap of 100 bp
 * 2438 3161: contig of 724 bp in length
 * 3162 3261: gap of 100 bp
 * 3262 3956: contig of 705 bp in length
 * 3957 4066: gap of 100 bp
 * 4067 4772: contig of 706 bp in length
 * 4773 4872: gap of 100 bp
 * 4873 5564: contig of 692 bp in length
 * 5565 5664: gap of 100 bp
 * 5665 6357: contig of 733 bp in length
 * 6358 6497: gap of 100 bp
 * 6498 7202: contig of 705 bp in length
 * 7203 7302: gap of 100 bp
 * 7303 8028: contig of 726 bp in length
 * 8029 8128: gap of 100 bp
 * 8129 8803: contig of 675 bp in length
 * 8804 8903: gap of 100 bp
 * 8904 9613: contig of 710 bp in length
 * 9614 9713: gap of 100 bp
 * 9714 10409: contig of 696 bp in length
 * 10410 10509: gap of 100 bp
 * 10510 11237: contig of 728 bp in length
 * 11238 11337: gap of 100 bp
 * 11338 12043: contig of 706 bp in length
 * 12044 12143: gap of 100 bp
 * 12144 12857: contig of 724 bp in length
 * 12858 12967: gap of 100 bp
 * 12968 13660: contig of 693 bp in length
 * 13661 13760: gap of 100 bp
 * 13761 14489: contig of 729 bp in length
 * 14490 14589: gap of 100 bp
 * 14590 15314: contig of 725 bp in length
 * 15315 15414: gap of 100 bp
 * 15415 16129: contig of 715 bp in length
 * 16130 16229: gap of 100 bp
 * 16230 16946: contig of 717 bp in length
 * 16947 17046: gap of 100 bp
 * 17047 17769: contig of 723 bp in length
 * 17770 17869: gap of 100 bp
 * 17870 18574: contig of 705 bp in length
 * 18575 18674: gap of 100 bp
 * 18675 19379: contig of 705 bp in length
 * 19380 19479: gap of 100 bp
 * 19480 20186: contig of 707 bp in length
 * 20187 20286: gap of 100 bp
 * 20287 20980: contig of 694 bp in length
 * 20981 21080: gap of 100 bp
 * 21081 21779: contig of 699 bp in length

* 21780 21879: gap of 100 bp
 * 21880 22594: contig of 715 bp in length
 * 22595 22694: gap of 100 bp
 * 22695 23399: contig of 705 bp in length
 * 23400 23499: gap of 100 bp
 * 23500 24217: contig of 718 bp in length
 * 24218 24317: gap of 100 bp
 * 24318 25026: contig of 709 bp in length
 * 25027 25126: gap of 100 bp
 * 25127 25836: contig of 710 bp in length
 * 25837 25936: gap of 100 bp
 * 25937 26637: contig of 701 bp in length
 * 26638 26737: gap of 100 bp
 * 26738 27446: contig of 709 bp in length
 * 27447 27546: gap of 100 bp
 * 27547 28274: contig of 728 bp in length
 * 28275 28374: gap of 100 bp
 * 28375 29095: contig of 721 bp in length
 * 29096 29195: gap of 100 bp
 * 29196 29917: contig of 722 bp in length
 * 29918 30017: gap of 100 bp
 * 30018 30724: contig of 707 bp in length
 * 30725 30824: gap of 100 bp
 * 30825 31523: contig of 705 bp in length
 * 31530 31629: gap of 100 bp
 * 31630 32324: contig of 695 bp in length
 * 32325 32424: gap of 100 bp
 * 32425 33116: contig of 692 bp in length
 * 33117 33216: gap of 100 bp
 * 33217 33936: contig of 720 bp in length
 * 33937 34036: gap of 100 bp
 * 34037 34750: contig of 714 bp in length
 * 34751 34850: gap of 100 bp
 * 34851 35578: contig of 728 bp in length
 * 35579 35678: gap of 100 bp
 * 35679 36393: contig of 715 bp in length
 * 36394 36493: gap of 100 bp
 * 36494 37203: contig of 710 bp in length
 * 37204 37303: gap of 100 bp
 * 37304 37965: contig of 662 bp in length
 * 37966 38065: gap of 100 bp
 * 38066 38761: contig of 716 bp in length
 * 38762 38861: gap of 100 bp
 * 38862 39550: contig of 709 bp in length
 * 39591 39690: gap of 100 bp
 * 39691 40403: contig of 713 bp in length
 * 40404 40503: gap of 100 bp
 * 40504 41238: contig of 735 bp in length
 * 41239 41338: gap of 100 bp
 * 41339 42064: contig of 726 bp in length
 * 42065 42164: gap of 100 bp
 * 42165 42880: contig of 716 bp in length
 * 42881 42980: gap of 100 bp
 * 42981 43687: contig of 707 bp in length
 * 43688 43787: gap of 100 bp
 * 43788 44504: contig of 717 bp in length
 * 44505 44604: gap of 100 bp
 * 44605 45307: contig of 703 bp in length
 * 45308 45407: gap of 100 bp
 * 45408 46105: contig of 699 bp in length
 * 46107 46206: gap of 100 bp
 * 46207 46903: contig of 703 bp in length
 * 46910 47009: gap of 100 bp
 * 47010 47696: contig of 687 bp in length
 * 47697 47796: gap of 100 bp
 * 47797 48531: contig of 735 bp in length
 * 48532 48631: gap of 100 bp
 * 48632 49341: contig of 710 bp in length
 * 49342 49441: gap of 100 bp
 * 49442 50163: contig of 721 bp in length
 * 50163 50262: gap of 100 bp
 * 50263 50990: contig of 728 bp in length
 * 50991 51090: gap of 100 bp

[illegible]

	* 51091	51803: contig of 713 bp in length	
*	51804	51903: gap of 100 bp	
*	51904	52610: contig of 707 bp in length	
*	52611	52710: gap of 100 bp	
*	52711	53412: contig of 702 bp in length	
*	53413	53512: gap of 100 bp	
*	53513	54253: contig of 741 bp in length	
*	54254	54353: gap of 100 bp	
*	54354	55084: contig of 731 bp in length	
*	55085	55184: gap of 100 bp	
*	55185	55972: contig of 788 bp in length	
*	55973	56072: gap of 100 bp	
*	56073	56855: contig of 783 bp in length	
*	56856	56955: gap of 100 bp	
*	56956	57708: contig of 753 bp in length	
*	57709	57808: gap of 100 bp	
*	57809	58579: contig of 771 bp in length	
*	58580	58679: gap of 100 bp	
Query Match		53.6%; Score 612; DB 2; Length 214212;	
Best Local Similarity		82.3%; Pred. No. 1.7e-161;	
Matches 633; Conservative		0; Mismatches 136; Indels 0; Gaps 0;	
QY	1	AGATAGCAGACGAGAGAACAACCAGCTCCGGTTTCAGGTCTTCTCGTAGGCTGATTGC	60
Db	168605	AGATAACACACGACGAGACCAACCAGCTCTCTTTTCAGGTCTTCTCGTAGGCTGATTGC	168546
QY	61	GCTGGAAAGGGAGTAGTGCCCAACCAATGAAGAAGCTGTGGAGACAGGAGGACAAGAAC	120
Db	168545	GCTGGAAAGGGAGTAGTGCCGCCCAAATGAAGAAGCTGTGGGAACAGGAGGACAAGAAC	168486
QY	121	AGGCTCACGAGNAGANTTCAGACGACGAGTGCCTACTCTCTTTTCTTTTGTCTCTTTTT	180
Db	168485	AGGCTCACGAGNAGANTTCAGACGACGAGTGCCTACTCTCTTTTCTTTTGTCTCTTTTT	168426
QY	181	GCTCTGTCAACCAGGCTGAAGTACAGATGCTGTAGTCTACGGCTCACTGCGCTTGACCTC	240
Db	168425	GCTCTGTCAACCAGGCTGAAGTACAGTGTAGTCTACGGCTCACTGCGCTTGACCTC	168366
QY	241	CGAGCTCAAGTGATTCCTCTGCTCAGCTTTCGAAGTAACTGGGACACAGGCAATGCAT	300
Db	168365	CGAGCTCAAGTGATTCCTCTGCTCAGCTTTCGAAGTAACTGGGACACAGGCAATGCAT	168305
QY	301	CACCAAGCTAGGCTAATGTTTATATTTTGTAGAGATGGGTCTCAACATGTTGCCCA	360
Db	168305	CACCAAGCTAGGCTAATGTTTATATTTTGTAGAGATGGGTCTCAACATGTTGCCCA	168246
QY	361	GGTTGGTCTCAAACTCTCGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAGATGCTGG	420
Db	168245	GGTTGGTCTCAAACTCTCGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAGATGCTGG	168186
QY	421	GAATTAAGCGGTGAGCCACCGGCGCAGGCTCAGTAATCTTAATCACAGGATTTTAAAAA	480
Db	168185	GAATTAAGCGGTGAGCCACCTCGCAGGCTGAGTAATCTTAATCACAGGATTTTAAAAA	168126
QY	481	GAATTAAGCGGTGAGCCACCATTAACCAATATCTCTTACCAATTTGGTAGTAATATTG	540
Db	168125	GAATTAAGCGGTGAGCCACCATTAACCAATATCTCTTACCAATTTGGTAGTAATATTG	168066
QY	541	CTAATAGTACCTAATTTTGTAGTAGGACCTGTTTATACATATATCCATTCCTCTCTTTT	600
Db	168065	CTAATAGTACCTAATTTTGTAGTAGGACCTGTTTATACATATATCCATTCCTCTCTTTT	168006
QY	601	TTCATTTGCTTTCTGTTTAAATGGGACGCTACCTCTCTTGGCATCTAGCAGAAATGAGCTCG	660
Db	168005	TTCATTTGCTTTCTGTTTAAATGGGACGCTACCTCTTGGCATCTAGCAGAAATGAGCTCG	167946
QY	661	TGCAGTTTACAAAAAGAAATGAGATCAGAGTACTTTTTGTGCCACCAACGTCGTCTGAG	720
Db	167945	NN	167886
QY	721	AAATTTGAGTGTTACTATCATCACATTTACTTTTATTTTATCTCGAATA	769

* 4873 5564: contig of 692 bp in length
 * 5565 5664: gap of 100 bp
 * 5665 6397: contig of 733 bp in length
 * 6398 6497: gap of 100 bp
 * 6498 7202: contig of 705 bp in length
 * 7203 7302: gap of 100 bp
 * 7303 8028: contig of 726 bp in length
 * 8029 8128: gap of 100 bp
 * 8129 8803: contig of 675 bp in length
 * 8804 8903: gap of 100 bp
 * 8904 9613: contig of 710 bp in length
 * 9614 9713: gap of 100 bp
 * 9714 10409: contig of 696 bp in length
 * 10410 10509: gap of 100 bp
 * 10510 11237: contig of 728 bp in length
 * 11238 11337: gap of 100 bp
 * 11338 12043: contig of 706 bp in length
 * 12044 12143: gap of 100 bp
 * 12144 12867: contig of 724 bp in length
 * 12868 12967: gap of 100 bp
 * 12968 13660: contig of 693 bp in length
 * 13661 13760: gap of 100 bp
 * 13761 14489: contig of 729 bp in length
 * 14490 14589: gap of 100 bp
 * 14590 15314: contig of 725 bp in length
 * 15315 15414: gap of 100 bp
 * 15415 16129: contig of 715 bp in length
 * 16130 16229: gap of 100 bp
 * 16230 16946: contig of 717 bp in length
 * 16947 17046: gap of 100 bp
 * 17047 17769: contig of 723 bp in length
 * 17770 17869: gap of 100 bp
 * 17870 18574: contig of 705 bp in length
 * 18575 18674: gap of 100 bp
 * 18675 19379: contig of 705 bp in length
 * 19380 19479: gap of 100 bp
 * 19480 20186: contig of 707 bp in length
 * 20187 20286: gap of 100 bp
 * 20287 20980: contig of 694 bp in length
 * 20981 21080: gap of 100 bp
 * 21081 21779: contig of 699 bp in length
 * 21780 21879: gap of 100 bp
 * 21880 22594: contig of 715 bp in length
 * 22595 22694: gap of 100 bp
 * 22695 23399: contig of 705 bp in length
 * 23400 23499: gap of 100 bp
 * 23500 24217: contig of 718 bp in length
 * 24218 24317: gap of 100 bp
 * 24318 25026: contig of 709 bp in length
 * 25027 25126: gap of 100 bp
 * 25127 25836: contig of 710 bp in length
 * 25837 25936: gap of 100 bp
 * 25937 26637: contig of 701 bp in length
 * 26638 26737: gap of 100 bp
 * 26738 27446: contig of 709 bp in length
 * 27447 27546: gap of 100 bp
 * 27547 28274: contig of 728 bp in length
 * 28275 28374: gap of 100 bp
 * 28375 29095: contig of 721 bp in length
 * 29096 29195: gap of 100 bp
 * 29196 29917: contig of 722 bp in length
 * 29918 30017: gap of 100 bp
 * 30018 30724: contig of 707 bp in length
 * 30725 30824: gap of 100 bp
 * 30825 31529: contig of 705 bp in length
 * 31530 31629: gap of 100 bp
 * 31630 32324: contig of 695 bp in length
 * 32325 32424: gap of 100 bp
 * 32425 33116: contig of 692 bp in length
 * 33117 33216: gap of 100 bp
 * 33217 33936: contig of 720 bp in length
 * 33937 34036: gap of 100 bp
 * 34037 34750: contig of 714 bp in length

* 34751 34850: gap of 100 bp
 * 34851 35578: contig of 728 bp in length
 * 35579 35678: gap of 100 bp
 * 35679 36393: contig of 715 bp in length
 * 36394 36493: gap of 100 bp
 * 36494 37203: contig of 710 bp in length
 * 37204 37303: gap of 100 bp
 * 37304 37965: contig of 662 bp in length
 * 37966 38065: gap of 100 bp
 * 38066 38781: contig of 716 bp in length
 * 38782 38881: gap of 100 bp
 * 38882 39590: contig of 709 bp in length
 * 39591 39690: gap of 100 bp
 * 39691 40403: contig of 713 bp in length
 * 40404 40503: gap of 100 bp
 * 40504 41238: contig of 735 bp in length
 * 41239 41338: gap of 100 bp
 * 41339 42054: contig of 726 bp in length
 * 42055 42164: gap of 100 bp
 * 42165 42880: contig of 716 bp in length
 * 42881 42980: gap of 100 bp
 * 42981 43687: contig of 707 bp in length
 * 43688 43787: gap of 100 bp
 * 43788 44504: contig of 717 bp in length
 * 44505 44604: gap of 100 bp
 * 44605 45307: contig of 703 bp in length
 * 45308 45407: gap of 100 bp
 * 45408 46106: contig of 699 bp in length
 * 46107 46206: gap of 100 bp
 * 46207 46909: contig of 703 bp in length
 * 46910 47009: gap of 100 bp
 * 47010 47696: contig of 687 bp in length
 * 47697 47796: gap of 100 bp
 * 47797 48511: contig of 735 bp in length
 * 48512 48611: gap of 100 bp
 * 48612 49341: contig of 710 bp in length
 * 49342 49441: gap of 100 bp
 * 49442 50162: contig of 721 bp in length
 * 50163 50262: gap of 100 bp
 * 50263 50990: contig of 728 bp in length
 * 50991 51090: gap of 100 bp
 * 51091 51803: contig of 713 bp in length
 * 51804 51903: gap of 100 bp
 * 51904 52610: contig of 707 bp in length
 * 52611 52710: gap of 100 bp
 * 52711 53412: contig of 702 bp in length
 * 53413 53512: gap of 100 bp
 * 53513 54253: contig of 741 bp in length
 * 54254 54353: gap of 100 bp
 * 54354 55084: contig of 731 bp in length
 * 55085 55184: gap of 100 bp
 * 55185 55972: contig of 788 bp in length
 * 55973 56072: gap of 100 bp
 * 56073 56855: contig of 783 bp in length
 * 56856 56955: gap of 100 bp
 * 56956 57708: contig of 753 bp in length
 * 57709 57808: gap of 100 bp
 * 57809 58579: contig of 771 bp in length
 * 58580 58679: gap of 100 bp

Query Match 38.4%; Score 437.6; DB 2; Length 214212;
 Best Local Similarity 78.7%; Pred. No. 4e-112;
 Matches 463; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 1 AGATAAGCACACGACAGAGAGCAACAGCTCCCTTTTCAGGTCCTTCTCAGGCTGATTCCG 60
 |||||
 DB 7551 AGATAAGCACACGACAGAGAGCAACAGCTCCCTTTTCAGGTCCTTCTCAGGCTGATTCCG 7610
 |||||
 QY 61 GCTGGAAGGGAGTAGGTCCTCCCAATGAAGAGCTGTGGGAAGACAGGACGACAGAAC 120
 |||||
 DB 7611 GCTGGAAGGGAGTAGTGTCCCGCAATGAAGAGCTGTGGGAAGACAGGACGACAGAAC 7670
 |||||
 QY 121 AGGCTCCACGAGAGAGATTTTCAGAGCAGAGCTCGTACTCTTTTCTTTTCTTTTCTTTT 180

RP11-205K6 is from the library RPII-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-205K6. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-123K19 is at 42256 in this sequence. The true right end of clone RP11-494N15 is at 2000 in this sequence.

Location/Qualifiers

1. 44255

/organism="Homo sapiens"

/db xref="taxon:9606"

/chromosome="9"

/clone="RP11-205K6"

/clone_lib="RPII-11.1"

/clone 11485 a 11569 c 10681 g 10520 t

BASE COUNT 11485 a 11569 c 10681 g 10520 t

ORIGIN

Query Match 17.8%; Score 203.4; DB 9; Length 44255;

Best Local Similarity 65.1%; Pred. No. 5.1e-46;

Matches 300; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

QY 161 TTTTCTTTTGTGTTTCTGCTGTCACCCAGGCTGAAGTACAGTGGTTAGTCTACGG 220

Db 33974 TTTTCTTTGAGACAGGGTTTGTCTGTTGCCAGGCTGGAGTGCAGTGGTGTGATCATGA 33915

QY 221 CTCACTGAGCTTTGACCTCCAGGCTCAAGTGTATCTCTGCTCAGCTTTTCCAAAGTAA 280

Db 33914 CTCACTGAGGCTCAACCTTCCGGGCTCAAGAGATCTCTTCTCAGCTTCCCAAGTAG 33855

QY 281 CTGGGACCAAGGATGATCACCACGCTAGGCTATTTTGTAGAGATG 340

Db 33854 CTGAGACCAAGGCTGACACCATGTGTGCTTAATTTTAAAGTTTGTAGAGATA 33795

QY 341 GGGTCTCACCATTGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGG 400

Db 33794 GGGTCTCTCTATGTTGCCCAAGCTGGTCTGAACCTCTGGGCTCAAACTCTGCCCCACC 33735

QY 401 TCAACTCTCCCAATGCTGGGATACAGGCTGAGCCACCGGCGGAGGCTGAGTAATCC 460

Db 33734 TCAAGCTCTCCCAAGTGTGGGATACAGGCGGAGGCTGCTGCTGCCCATTTAATAC 33675

QY 461 TAATCAGAGGATTTTAAAGAAAGAACTTCTGCGCCACCCATTAACAATATCTCTACCA 520

Db 33674 TTTTAAATGCGCTTTTATAAGTGGGATTTCCCAATATATTTTCAAACTGCTTGTATTAA 33615

QY 521 ATTTGGTAGTAATATTTTGTCTAATAGTACCTAATTTTAGGTAGGCACTGTGTTTATAC 580

Db 33614 AATATAGAAACTTACTTATTTCTGCTTTTCTTAATTTTCTGTAGCCATTTTGCCAAACC 33555

QY 581 ATATATCCATTCCTCTTTTGTGATGCTTTCTGTTTAAAT 621

Db 33554 CCTTTTGTAGTCTTAATAATTTCTAAATGATTATTGAT 33514

RESULT 9

AC079927/c

LOCUS AC079927 84577 bp DNA linear PRI 21-FEB-2002

DEFINITION Homo sapiens BAC clone RP11-702A23 from 4, complete sequence.

ACCESSION AC079927

VERSION AC079927.5 GI:18071472

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Sulston, J.E. and Waterston, R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

7671 ACGCTCCAGAGAGATTTCAGAGCAGAGCTGCGTACTCTTTTCTTTTGTGTTCTTTT 7730

QY 181 GCTCTGTACCCAGGCTGAAGTACAGTGGTGTAGCTCAGGCTCAGCTGAGCTTTGACCTC 240

Db 7731 GCTCTGTACCCAGGCTGAAGTACAGTGGTGTAGCTCAGGCTCAGCTGAGCTTTGACCTC 7790

QY 241 CAGGCTCAAGTGATCTCTGCTCAGCTTTTCCAAAGTAACTGGGACCAAGGATGAT 300

Db 7791 CACGCTCAAGTGATCTCTGCTCAGCTTTTCCAAAGTAACTGGGACCAAGGATGAT 7850

QY 301 CACCACTGAGTATGTTTACATTTTGTAGAGATGGGCTCTCACCATTGTTGCCA 360

Db 7851 CACCACTGAGTATGTTTACATTTTGTAGAGATGGGCTCTCACCATTGTTGCCA 7910

QY 361 GGTGTGTCAAACTCTCTGGGCTCAAGCAATCGCTCAGCTCAACCTCCCAAAATGCTGG 420

Db 7911 CGTTGTCTCAAACTCTCTGGGCTCAAGCAATCGCTCAGCTCAACCTCCCAAAATGCTGG 7970

QY 421 GATTACAGG-CGTGAGCCACCGGCGGAGGCTGAGTAATCTTAATCAGAGATTTTAAA 479

Db 7971 GATTACAGGCGGTGAGCCACCGGCGGAGGCTGAGTAATCTTAATCAGAGATTTTAAA 8030

QY 480 AGAACTTCTGCGGCGCACCAATTAACAATATCTCTCAACATTTGCTAGTAATATTT 539

Db 8031 NNN 8090

QY 540 GCTAATAGTACCTAATTTTGTAGTGGCTGTTTATACATATATC 587

Db 8091 NNN 8138

RESULT 8

AL356309/c

LOCUS AL356309 44255 bp DNA linear PRI 18-JAN-2002

DEFINITION Human DNA sequence from clone RP11-205K6 on chromosome 9, complete sequence.

ACCESSION AL356309

VERSION AL356309.23 GI:18375796

KEYWORDS HTG.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Sehra, H.

JOURNAL Direct Submission

COMMENT Submitted (18-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 25, 2002 this sequence version replaced gi:16973835. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/chr9>

```

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 84577)
Cedroni,M., Abbott,A. and Boyer,E.
Unpublished (2001)
3 (bases 1 to 84577)
Waterston,R.H.
Direct Submission
Submitted (17-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 84577)
Waterston,R.H.
Direct Submission
Submitted (05-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 84577)
Waterston,R.
Direct Submission
Submitted (30-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 84577)
Waterston,R.
Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 5, 2002 this sequence version replaced gi:16924160.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
-----
Center project name: H_NH0702A23
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-757K22, 2000 bp overlap;
the clone sequenced to the right is RP11-19F13. Actual start of
this clone is at base position 110812 of RP11-757K22; actual end is
at base position 84577 of RP11-702A23.

Two transposons occurred in the growth of the clone that have been

```

```

omitted from the finished sequence.
FEATURES
source
Location/Qualifiers
1..84577
/organism="Homo sapiens"
/dbxref="taxon:9606"
/chromosomes="4"
/map="4"
/clone="RP11-702A23"
/clone_lib="RPCI-11"
1..206
/repeat_region
/rept_family="Alu"
256..528
/repeat_region
/rept_family="Alu"
697..723
/repeat_region
/rept_family="(TTTC)n"
713..846
/repeat_region
/rept_family="Alu"
1407..1747
/repeat_region
/rept_family="MER1_type"
1799..2262
/repeat_region
/rept_family="L2"
2265..2290
/repeat_region
/rept_family="(TTTAA)n"
2266..2574
/repeat_region
/rept_family="Alu"
2599..2719
/repeat_region
/rept_family="Alu"
2891..2996
/repeat_region
/rept_family="MIR"
3255..3607
/repeat_region
/rept_family="MER2_type"
3620..3713
/repeat_region
/rept_family="MERS3"
3637..3719
/repeat_region
/rept_family="MERS3"
4055..4083
/repeat_region
/rept_family="AT_rich"
4056..4358
/repeat_region
/rept_family="Alu"
4698..4721
/repeat_region
/rept_family="AT_rich"
5095..5462
/repeat_region
/rept_family="MaLR"
6970..7010
/repeat_region
/rept_family="(TTC)n"
6985..7294
/repeat_region
/rept_family="Alu"
7703..7992
/repeat_region
/rept_family="Alu"
8526..8559
/repeat_region
/rept_family="(T)n"
8532..8840
/repeat_region
/rept_family="Alu"
9438..9458
/repeat_region
/rept_family="AT_rich"
9440..9738
/repeat_region
/rept_family="Alu"
9744..9886
/repeat_region
/rept_family="MIR"
10404..10507
/repeat_region
/rept_family="L2"
11088..11207
/repeat_region
/rept_family="L2"
11215..11528
/repeat_region
/rept_family="Alu"
11501..11662
/repeat_region
/rept_family="GA-rich"
11639..11846
/repeat_region
/rept_family="L2"
11847..11971
/repeat_region
/rept_family="Alu"
11972..12012
/repeat_region
/rept_family="L2"

```


of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Apr 30, 2002 this sequence version replaced gi:20335973.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

Location/Qualifiers

1. .143721
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="3"
 /clone="RP11-48714"

misc_feature

1. .2005
 /notes="overlaps bases 165133..167137 of clone AC068631"

/function="clone overlap"

141..401

/rpt_family="MER102"

complement(505..809)

/rpt_family="AluJb"

complement(1770..2080)

/rpt_family="AluSg"

complement(2157..2196)

/rpt_family="MIR"

4503..4538

/rpt_family="AT-rich"

complement(5204..5263)

/rpt_family="L1M4"

complement(5264..5573)

/rpt_family="AluSg"

complement(5574..5724)

/rpt_family="L1M4"

complement(6108..6595)

/rpt_family="HAL1"

complement(6764..7058)

/rpt_family="AluSg"

complement(7109..7268)

/rpt_family="HAL1"

complement(7824..8136)

repeat_region
 complement(8820..8946)
 /rpt_family="MER31A"
 repeat_region
 complement(8947..9869)
 /rpt_family="MER31-internal"
 repeat_region
 9870..10054
 /rpt_family="(TTTC)n"
 repeat_region
 complement(10055..10338)
 /rpt_family="AluSp"
 repeat_region
 complement(10339..10520)
 /rpt_family="MER31-internal"
 repeat_region
 complement(10521..10545)
 /rpt_family="L1M42"
 repeat_region
 10546..10576
 /rpt_family="(TA)n"
 repeat_region
 complement(10577..10695)
 /rpt_family="L1M42"
 repeat_region
 complement(10696..10969)
 /rpt_family="AluYa5"
 repeat_region
 complement(10970..11174)
 /rpt_family="L1M42"
 repeat_region
 complement(11175..11480)
 /rpt_family="AluSg"
 repeat_region
 complement(11481..11855)
 /rpt_family="L1M42"
 repeat_region
 complement(11856..12141)
 /rpt_family="MER31-internal"
 repeat_region
 complement(12142..12553)
 /rpt_family="MLT1B"
 repeat_region
 complement(12554..13417)
 /rpt_family="MER31-internal"
 repeat_region
 complement(13418..14345)
 /rpt_family="L1M44"
 repeat_region
 14351..14422
 /rpt_family="AluSg/x"
 repeat_region
 complement(14443..15165)
 /rpt_family="L1M44"
 repeat_region
 complement(15166..15181)
 /rpt_family="AluY"
 repeat_region
 15182..15231
 /rpt_family="(TTTA)n"
 repeat_region
 complement(15232..15514)
 /rpt_family="AluY"
 repeat_region
 complement(15515..15882)
 /rpt_family="L1M44"
 repeat_region
 complement(15883..16199)
 /rpt_family="AluJo"
 repeat_region
 complement(16200..16383)
 /rpt_family="L1M44"
 repeat_region
 complement(16520..17008)
 /rpt_family="MER31-internal"
 repeat_region
 complement(17057..17578)
 /rpt_family="MER31-internal"
 repeat_region
 complement(17579..17741)
 /rpt_family="MER31-internal"
 repeat_region
 complement(17769..17897)
 /rpt_family="MER31-internal"

Query Match 17.2%; Score 196.6; DB 9; Length 143721;

Best Local Similarity 74.6%; Pred. No. 5.8e-44;
 Matches 247; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 177 TTTTGTCTGTCCACCCAGGCTGAAGTACAGTGTGTTAGCTCACGGCTCAGTGCAGCTTTGA 236

Db 121424 TTTTGTCTGTCCACCCAGGCTGAAGTACAGTGTGTTAGCTCACGGCTCAGTGCAGCTTTGA 121365

QY 237 CTCCACAGGCTCAAGTACAGTGTGTTAGCTCACGGCTTTCCAAAGTAACATGGGACCAACAGGCAT 296

Db 121364 CTCCACAGGCTCAAGTACAGTGTGTTAGCTCACGGCTTTCCAAAGTAACATGGGACCAACAGGCAT 121305

QY 297 GCATCACCAGGCTAGGCTATGTTTGTACATTTTGTAGAGATGGGGTCTCACCATTGTTG 356

Db 121304 GCATCACCAGGCTAGGCTATGTTTGTACATTTTGTAGAGATGGGGTCTCACCATTGTTG 121245

357 CCAGGTTGGTCTCAAACTCCTGGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 416
 121244 CCAGGTTGGTCTCGAACTCCTGGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 121185
 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGGCTGAGTAATCTTAATACAGAGTTTGA 476
 121184 CTGAGATTACAGCGCTGAGCTACTGTCTGGCCAAAGTATGTGTTTTATCCCACTTT 121125
 477 AAAGAAATCTCTGGCCACCCATTAAACA 507
 121124 TAAGTGAAGAATCTGAGCCTCAAAATCACAGA 121094

RESULT 11
 LOCUS AK023951/c 2343 bp mRNA linear PRI 01-AUG-2002
 DEFINITION Homo sapiens cDNA FLJ13889 fis, clone THYRO1001595.
 ACCESSION AK023951
 VERSION AK023951.1 GI:10436049
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens thyroid gland cDNA to mRNA, clone lib:THYRO1 clone:THYRO1001595.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
 AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K., Tanai, H., Kinata, M., Watanabe, M., Hiracka, S., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y. and Kanehori, K.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2343)
 AUTHORS Isogai, T. and Otsuki, T.
 JOURNAL Direct Submission
 SUBMITTED (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing. Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology; Institute of Medical Science, University of Tokyo.

FEATURES
 source
 1..2343
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="THYRO1001595"
 /tissue_type="thyroid gland"
 /clone_lib="THYRO1"
 /note="cloning vector: pME18SFL3"
 BASE COUNT 603 a 515 c 535 g 690 t
 ORIGIN

Query Match 17.1%; Score 195; DB 9; Length 2343;
 Best Local Similarity 80.6%; Pred. No. 5.7e-44;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

177 TTTTGTCTGTCAACCCAGGCTGAAGTACAGTGGTGTAGCTCAGCGGTCTCACTGAGCTTTGA 236
 2331 TCTGTGTCTGTCAACCCAGGCTGAAGTACAGTGGTGTAGCTCAGCGGTCTCACTGAGCTTTGA 2272
 237 CTTCCAGGCTCAAGTGATCTCTCTCTCAGCTTTCCAGTAACTGGGACACAGGAT 296
 2271 CTTCCAGGCTCAGGTGATCTCTCCACCTCAGCGTCCGAGTAGTGGAGCTACAGGAT 2212
 297 GCATCACCAGCTAGGTATTTTACATTTTGTAGAGATGGGCTCTCACCATGTTG 356
 2211 GCACCACCGCTCAGCTAAATTTTGTACTTTTTGTAGAGCGGGTTTACCATGTTG 2152

357 CCAGGTTGGTCTCAAACTCCTGGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 416
 2151 CACAGGTTGGTCTCAGAACTCCTGGGCTCAAGCTCAAGCTCAACCTCCCAATG 2092
 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGGCTGAGTAATC 459
 2091 CTGGGATTACAACTGGGAGCCACCGTGGCCGCCGAGATCTC 2049

RESULT 12
 LOCUS AL133390 71872 bp DNA linear PRI 04-JAN-2001
 DEFINITION Human DNA sequence from clone RPI-317G22 on chromosome 1 Contains part of the KMO (kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)) gene, the CHML(choroideremia-like (Rab escort protein 2)) gene, the gene for encephalopsin, ESTs, STSs, GSSs and a CpG Island, complete sequence.

ACCESSION AL133390
 VERSION AL133390.7 GI:7406530
 KEYWORDS HTG.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 71872)
 AUTHORS Parker, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 REQUEST: clonerrequest@sanger.ac.uk

COMMENT On Apr 3, 2000 this sequence version replaced gi:7320611. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence is the entire insert of clone RPI-317G22 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri RPI-317G22 is from the library RPI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pCIPAC2. Location/Qualifiers
 1..71872
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RPI-317G22"
 /clone_lib="RPI-1"
 21..2548
 /note="LIPBb repeat: matches 30. 2559 of consensus"
 2509..2919
 /note="LIPBa repeat: matches 601. 1014 of consensus"
 2920..3281
 /note="THL1B repeat: matches 1. 364 of consensus"
 3282..4433
 /note="LIPBa repeat: matches -1481. 601 of consensus"
 4539..7775

FEATURES
 source
 1..71872
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /clone="RPI-317G22"
 /clone_lib="RPI-1"
 21..2548
 /note="LIPBb repeat: matches 30. 2559 of consensus"
 2509..2919
 /note="LIPBa repeat: matches 601. 1014 of consensus"
 2920..3281
 /note="THL1B repeat: matches 1. 364 of consensus"
 3282..4433
 /note="LIPBa repeat: matches -1481. 601 of consensus"
 4539..7775

```

/note="L1M1 repeat: matches -68. .3127 of consensus"
7784. .7869
/note="MER2 repeat: matches 130. .209 of consensus"
8165. .8424
/note="L1PA5 repeat: matches 5884. .6143 of consensus"
8425. .8631
/note="L1P2 repeat: matches 5392. .5600 of consensus"
9118. .9406
/note="AluSx repeat: matches 1. .286 of consensus"
complement(9535. .10007)
/note="match: GSS: Em:AQ882365"
9650. .9956
/note="AluSx repeat: matches 1. .311 of consensus"
10366. .10674
/note="AluJb repeat: matches 1. .307 of consensus"
10800. .10849
/note="25 copies 2 mer tt 76% conserved"
join(10853. .10910,12922. .13004,14186. .14287,14378. .14437.
16127. .19815)
/gene="KMO"
join(<10853. .10910,12922. .13004,14186. .14287,14378. .14437.
16127. .19815)
/gene="KMO"
/product="dJ317G22.1 (kynurenine 3-monooxygenase
(kynurenine 3-hydroxylase))"
/note="match: CDNAS: Em:AF056031 Em:AF056032 Em:Y13153
match: ESTs: Em:AI074145 Em:R64497 Em:AI341967 Em:HA7435
Em:R65593"
/evidence=not_experimental
join(<10853. .10910,12922. .13004,14186. .14287,14378. .14437.
16127. .16327)
/gene="KMO"
Tr:076150"
/note="match: proteins: Tr:O15229 Tr:O88867 Tr:Q21795
/codon_start=1
/evidence=not_experimental
/product="dJ317G22.1 (kynurenine 3-monooxygenase
(kynurenine 3-hydroxylase))"
/protein_id="CAC19783.1"
/db_xref="GI:12043384"
/translation="GFEDCLVFPDLMDKSNDSLCLPVFSRLRPDDHAIISDLSMYN
IEMRAHVNSWFIQKNRQFLHAMPSTFIPLYMTVTSRIRYHEAVQRWHWKKY
INGLFLGLSLIAISSTYLLIHYMSPRFLRLRPWNWIAHFNTTCPPAKAVDSLEQ
ISNLSIR"
11252. .11551
/note="MER1B repeat: matches 36. .329 of consensus"
11641. .11916
/note="AluSx repeat: matches 2. .292 of consensus"
complement(11977. .12463)
/note="match: GSS: Em:AQ358898"
complement(12102. .12365)
/note="match: STS: Em:G38435"
12194. .12418
/note="MIR repeat: matches 33. .258 of consensus"
12484. .12929
/gene="KMO"
/note="match: GSS: Em:AQ814890"
12485. .12534
/note="25 copies 2 mer tt 84% conserved"
complement(16125. .16461)
/note="match: STS: Em:G28193"
complement(16150. .16461)
/note="match: STS: Em:G25963"
complement(16804. .17103)
/note="match: STS: Em:G07828"
16807. .16985
/gene="KMO"
/note="match: GSS: Em:AQ527676"
16815. .16985
/gene="KMO"
/note="match: GSS: Em:AQ528204"
complement(16819. .16975)
/note="match: STS: Em:G08342"

```


ORIGIN

Query Match 17.1%; Score 195; DB 2; Length 147259;
 Best Local Similarity 80.6%; Pred. No. 1.7e-43;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 177 TTTTGTCTCTACCCAGGCTGAAGTACAGTGTAGCTCAGCGTCACTGCGAGCTTTGA 236
 Db 141121 TCTTGTCTCTACCCAGGAGTGCAGTGGCAGCATCACTGCTCACTGCGAGCTTTGA 141180
 QY 237 CTTCCAGGCTCAAGTATCTCTCGTCTCAGCTTTCCAGTAACTGGGACACACGCGAT 296
 Db 141181 CTTCCAGGCTCAGGTATCTCTCCACCTCAGCTCCGAGTACGCTGAGCTACAGCAT 141240
 QY 297 GCATCACCCAGCTAGGCTATTTTACATTTTGTAGAGATGGGCTCTCACCATTGTTG 356
 Db 141241 GCACCAACCCAGCTCAGCTAATTTTGTACTTTTGTAGAGAGCGGTTTCCACATGTTG 141300
 QY 357 CCAGGTTGGTCTCAACTCTCTGGCTCAAGCAATCGGCTCAGTCAACTCTCCCAATG 416
 Db 141301 CACAGCTGGTCTCAGACTCTCTGGGCTCAAGCTATCGGCTGCTCGGCTCCCAAGTG 141360
 QY 417 CTGGATTACAGCGCTGAGCCACCGGCGGAGGCTGAGTAATC 459
 Db 141361 CTGGATTACAGCTGGAGCCACCGTGGCGGCCGAGATCTC 141403

RESULT 14

AL365215

LOCUS

DEFINITION Human DNA sequence from clone RP11-41608 on chromosome 10, complete

ACCESSION

AL365215

VERSION

AL365215.23

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Ashwell, R.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonesrequest@sanger.ac.uk

On Jun 22, 2001 this sequence version replaced gi:14456224.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em.; EMBL; SW;

SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human

chromosome 10, constructed by the Sanger Centre Chromosome 10

Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr10

RP11-41608 is from the library RP11-11.2 constructed by the group

of Pieter de Jong. For further details see

http://www.chori.org/bacpac/home.htm

VECTOR: pBACe3.6

FEATURES

source

Location/Qualifiers
 1. .184703
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-41608"
 /clone_lib="RPC1-11.2"
 781. .1138

repeat_region

/note="MLT1A2 repeat: matches 3. .374 of consensus"
 1378. .1520

repeat_region

/note="MIR repeat: matches 13. .169 of consensus"
 1700. .2027

repeat_region

/note="AluSx repeat: matches 1. .311 of consensus"
 3259. .3643

repeat_region

/note="MLT1B repeat: matches 1. .390 of consensus"
 4028. .4397

repeat_region

/note="THE1C repeat: matches 1. .371 of consensus"
 4334. .5497

repeat_region

/note="LIME repeat: matches 866. .1405 of consensus"
 5955. .6285

repeat_region

/note="LIMEC repeat: matches 1813. .2148 of consensus"
 6335. .6655

repeat_region

/note="LIM4 repeat: matches 2690. .3056 of consensus"
 6856. .6959

repeat_region

/note="AluY repeat: matches 1. .299 of consensus"
 6960. .7059

repeat_region

/note="LIM4 repeat: matches 3056. .3146 of consensus"
 7199. .7937

repeat_region

/note="LIP48 repeat: matches 5420. .6156 of consensus"
 7950. .8103

repeat_region

/note="AluY repeat: matches 158. .311 of consensus"
 8106. .8401

repeat_region

/note="AluSp repeat: matches 1. .304 of consensus"
 8420. .8744

repeat_region

/note="LIM4 repeat: matches 3412. .3788 of consensus"
 8760. .9351

repeat_region

/note="LIM4 repeat: matches 3904. .5041 of consensus"
 9847. .10012

repeat_region

/note="LIMB7 repeat: matches 5979. .6149 of consensus"
 10161. .10335

repeat_region

/note="L2 repeat: matches 2019. .2198 of consensus"
 11843. .11895

repeat_region

/note="MIR repeat: matches 85. .145 of consensus"
 12341. .12649

repeat_region

/note="AluJo repeat: matches 1. .309 of consensus"
 13711. .13861

repeat_region

/note="MIR repeat: matches 99. .257 of consensus"
 13868. .14232

repeat_region

/note="THE1B repeat: matches 1. .364 of consensus"
 14240. .14328

repeat_region

/note="MIR repeat: matches 1. .92 of consensus"
 15157. .15178

repeat_region

/note="L1 copies 2 mer tt 100% conserved"
 15659. .16253

repeat_region

/note="L2 repeat: matches 1536. .2155 of consensus"
 16254. .16535

repeat_region

/note="AluJo repeat: matches 13. .293 of consensus"
 16536. .16584

repeat_region

/note="L2 repeat: matches 2155. .2201 of consensus"
 16585. .17051

repeat_region

/note="MLT1D repeat: matches 24. .505 of consensus"
 17056. .17346

repeat_region

/note="L2 repeat: matches 2196. .2489 of consensus"
 17471. .17519

repeat_region

/note="L2 repeat: matches 2660. .2708 of consensus"
 18417. .18641

repeat_region

/note="MIR repeat: matches 14. .262 of consensus"
 19232. .19341

repeat_region

/note="MER5B repeat: matches 1. .109 of consensus"
 19355. .19657

repeat_region

/note="AluJb repeat: matches 1. .303 of consensus"
 19935. .20010

repeat_region	52579..52808	/notes=AluJb repeat: matches 85..296 of consensus"
repeat_region	52845..53026	/notes=MGTA repeat: matches 221..425 of consensus"
repeat_region	53027..53391	/note=THE18 repeat: matches 1..363 of consensus"
repeat_region	53392..53493	/notes=MGTA repeat: matches 126..221 of consensus"
repeat_region	53494..53900	/notes=MLT2B repeat: matches 1..409 of consensus"

RESULT 15	AC090104	164167 bp	DNA	linear	HTG 06-AUG-2002
AC090104/c	Homo sapiens chromosome 8	Clone RP11-451E11	map 8,		
LOCUS	SEQUENCE	7	unordered pieces.		WORKING DRAFT
DEFINITION	AC090104				
ACCESSION	AC090104.4	GI:22123547			
VERSION	HTG: HTGS PHASE1:	HTGS DRAFT:	HTGS FULLTOP:		
KEYWORDS					

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 164167)
 Birren, B., Nusbaum, C. and Lander, E.
 Unpublished
 2 (bases 1 to 164167)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
 Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B., Brown, A.,
 Canarata, J., Campopiano, A., Chospel, Y., Colangelo, M., Collins, S.,
 Collymore, A., Cooke, P., DeArillano, K., Dewar, K., Diaz, J. S.,
 Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J.,
 Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagens, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
 Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T.,
 Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
 Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,
 McPherson, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
 Murphy, T., Taylor, J., Nguyen, C., Norbu, C., Norman, C. H.,
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,
 Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retica, R.,
 Riback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
 Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,
 Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 19:00:12 ; Search time 302 Seconds
(without alignments)
8508.378 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagagagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.:

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137.8	99.7	1141	18	Human maspin promo
2	745.4	65.3	12426	22	Tumour suppressor
3	723.4	63.4	12426	22	Tumour suppressor
4	195	17.1	568	22	Human cDNA clone (
5	195	17.1	2343	22	Human cDNA sequenc
6	190.2	16.7	66804	24	Human transporter
7	185.4	16.2	916	22	Human reproductive
8	185.4	16.2	32184	22	Human nervous syst
9	185.4	16.2	32184	22	Human nervous syst

10	185.4	16.2	38272	22	AAK84952	Human immune/haema
11	185.4	16.2	38348	22	AAK84953	Human immune/haema
12	184.6	16.2	240825	22	AAF24497	Human PG-3 gene.
13	184	16.1	1162	21	AAC79682	Human secreted pro
14	183.4	16.1	735	22	AAK05557	Human reproductive
15	183.4	16.1	735	22	AAK89703	Human digestive sy
16	182.8	16.0	227968	24	ABK83497	Human cDNA differe
17	182.6	16.0	1956	22	ABA21277	Human nervous syst
18	182.2	16.0	14748	24	ABK51275	Human Caspase-2, C
19	182.2	16.0	17026	22	AAK70372	Human immune/haema
20	181.4	15.9	17424	24	ABL68122	Ovary cancer relat
21	181.2	15.9	1519	20	AAZ10674	cDNA encoding a hu
22	181.2	15.9	103747	24	ABQ88139	Human osteoblast d
23	180.8	15.8	1421	22	AAK73297	Human immune/haema
24	180.4	15.8	21477	22	AAK66626	Human immune/haema
25	180.4	15.8	21480	22	AAK66625	Human immune/haema
26	180	15.8	21470	23	ABK42270	Genomic sequence #
27	179.8	15.8	1423	22	AAF27785	Human MANGO 347 co
28	179.8	15.8	1440	21	AAC90029	Clone HTHCW70 codi
29	179.8	15.8	1442	22	AAH33267	Human colon cancer
30	179.4	15.7	1248	24	AAH33244	Human secreted pro
31	179.2	15.7	5269	22	AAK80329	Human immune/haema
32	179	15.7	7233	22	AAK36623	Human cardiovascular
33	178.8	15.7	8053	22	AAI98931	Human kidney relat
34	178.8	15.7	8053	22	AAI63281	Human kidney relat
35	178.8	15.7	10241	22	AAK83768	Human immune/haema
36	178.8	15.7	10241	22	AAK33394	DNA encoding human
37	178.6	15.7	1125	22	ABA06543	Human cDNA SQ ID
38	178.6	15.7	1125	22	AAK28831	Human immunoglobul
39	178.6	15.7	66804	24	ABK87050	Human transporter
40	178.4	15.6	16181	22	AAK04268	Human reproductive
41	178.4	15.6	16181	23	ABK42539	Genomic sequence #
42	178	15.6	5962	23	AAK82348	DNA encoding novel
43	178	15.6	5962	23	AAK89334	DNA encoding novel
44	177.8	15.6	700	20	AAK30339	DNA encoding a hum
45	177.8	15.6	175737	24	ABK83571	Human cDNA differe

ALIGNMENTS

RESULT 1	
AAT89000	
ID	AAT89000 standard; cDNA; 1141 BP.
XX	
AC	AAT89000;
XX	
DT	22-APR-1998 (first entry)
DE	Human maspin promoter and partial coding cDNA.
XX	
KW	Maspin; serpin; mammary epithelial cell; human; promoter; malignant;
KW	tumour cell; treatment; prostate cancer; breast cancer; metastasis; ss.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	promoter
FT	Location/Qualifiers
FT	1..1141
FT	/*tag= a
FT	/note= "maspin promoter region"
FT	443..449
FT	/*tag= b
FT	/note= "Putative regulatory element AP2"
FT	451..457
FT	/*tag= c
FT	/note= "Putative regulatory element AP1"
FT	485..490
FT	/*tag= d
FT	/note= "Putative regulatory element Ets"
FT	684..691
FT	/*tag= e
FT	/note= "Putative regulatory element HRE"
FT	846..851

FT misc_signal /tag= f /note= "Putative regulatory element Ets" 420
FT 907...913 /tag= g /note= "Putative regulatory element APl" 480
FT prim_transcript 958...1141 /tag= h /note= "partial" 540
XX WO9736179-A1. 600
XX 02-OCT-1997. 600
XX 28-MAR-1997; 97WO-US05186. 660
XX 28-MAR-1996; 96US-0014368. 720
XX (DAND) DANA FARBER CANCER INST INC. 780
XX (DAND) DANA FARBER CANCER INST. 840
XX (PAR/) PARDEE A. 880
XX Sagar R, Zhang M; 900
XX WPI; 1997-489785/45. 960
XX Maspin gene promoter fragment - used to identify compounds for 1000
XX treatment of prostate or breast cancer 1080
XX Claim 4; Fig 3; Slpp; English. 1140
XX This sequence encodes the human maspin promoter region, including the 1200
XX transcription start site. Maspin is a serpin which is expressed in 1280
XX mammary epithelial cells. Its expression in these cells decreases 1360
XX with increasing malignancy and is lost in during metastasis. Maspin 1440
XX protein is also known to inhibit the mobility of tumour cells. This gene 1520
XX can be used in method for screening compounds to identify candidate 1600
XX compounds for the treatment of prostate cancer, or breast cancer. It can 1680
XX also be used to identify compounds that increase the expression of 1760
XX maspin, and for detecting the presence of metastatic prostate epithelial 1840
XX cells. 1920
SQ Sequence 1141 BP; 261 A; 292 C; 277 G; 311 T; 0 other; 2000
Query Match 99.7%; Score 1137.8; DB 18; Length 1141; 2080
Best Local Similarity 99.8%; Pred. No. 3.2e-301; 2160
Matches 1139; Conservative 0; Mismatches 2; Indels 0; Gaps 0; 2240
QY 1 AGATAAGCACAGCAGAGAGCAACAGCTCCGTTTTCAGGTCTCTTCTGAGGCTGATTGG 60
DB 1 AGATAAGCACAGCAGAGAGCAACAGCTCCGTTTTCAGGTCTCTTCTGAGGCTGATTGG 60
QY 61 GCTGGAAGGAGTAGGTCCCAACAAATGAAGAAGCTGTGGAGACAGAGGACAGAAC 120
DB 61 GCTGGAAGGAGTAGGTCCCAACAAATGAAGAAGCTGTGGAGACAGAGGACAGAAC 120
QY 121 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGGTACTCTTTCTTTTCTTTTCTTTT 180
DB 121 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGGTACTCTTTCTTTTCTTTTCTTTT 180
QY 181 GCTCTGTCCACGAGCTGAAGTACAGTGTGTTAGCTTCAGGCTCACTGCAGCTTTGACCTC 240
DB 181 GCTCTGTCCACGAGCTGAAGTACAGTGTGTTAGCTTCAGGCTCACTGCAGCTTTGACCTC 240
QY 241 CCAGGCTCAAGTGATCTCTGCTCAGCTTTCAGTAATCGGACCAAGGATCATCAT 300
DB 241 CCAGGCTCAAGTGATCTCTGCTCAGCTTTCAGTAATCGGACCAAGGATCATCAT 300
QY 301 CACCAAGCTAGGCTATTGTTTACATTTTTCAGAGATGGGCTCTCACCATTGTGCCCA 360
DB 301 CACCAAGCTAGGCTATTGTTTACATTTTTCAGAGATGGGCTCTCACCATTGTGCCCA 360
QY 361 GGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGTCAACTCCCAATGCTGG 420

DB 361 GGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGTCAACTCCCAATGCTGG 420
QY 421 GATTACAGGGCTGAGCCACCGGCGCAGGCTGAGTAATCTTAATCAGAGATTTTAAAAA 480
DB 421 GATTACAGGGCTGAGCCACCGGCGCAGGCTGAGTAATCTTAATCAGAGATTTTAAAAA 480
QY 481 GAAACTTCCTGCGCCACCCCAATTAACAATATCTCTTCCACCAATTTGGTAGTAATTTTG 540
DB 481 GAAACTTCCTGCGCCACCCCAATTAACAATATCTCTTCCACCAATTTGGTAGTAATTTTG 540
QY 541 CTAATAGTACCTAATTTTTHAGGTAGGACAGCTGTTTATACATATATATCCCTCTCTTTT 600
DB 541 CTAATAGTACCTAATTTTTHAGGTAGGACAGCTGTTTATACATATATATCCCTCTCTTTT 600
QY 601 TTGATTTCTTCTGTTTAAATGGCAGTACCTCTCTTGGCATCTAGCAGAAATGAGCTGC 660
DB 601 TTGATTTCTTCTGTTTAAATGGCAGTACCTCTCTTGGCATCTAGCAGAAATGAGCTGC 660
QY 661 TGCAGTTTACACAAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCCAACCAAGCTCTGAG 720
DB 661 TGCAGTTTACACAAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCCAACCAAGCTCTGAG 720
QY 721 AAATTTGTAGTGTACTATATACATACATTAATTTTATTTTATTCATCATATATTTACCTTCC 780
DB 721 AAATTTGTAGTGTACTATATACATACATTAATTTTATTTTATTCATCATATATTTACCTTCC 780
QY 781 GGTCTGCGTGGCGGAGAGGATTCGCTAGCGCATGTCTGTACGTATGTCATGTAACCTCAC 840
DB 781 GGTCTGCGTGGCGGAGAGGATTCGCTAGCGCATGTCTGTACGTATGTCATGTAACCTCAC 840
QY 841 AGCCCTCTCTGCGCCGAAACATGTTTGGAGGCTTTTGGAAAGCTGTGCGACCAACAGCACT 900
DB 841 AGCCCTCTCTGCGCCGAAACATGTTTGGAGGCTTTTGGAAAGCTGTGCGACCAACAGCACT 900
QY 901 TCAGCTGAATCATCTCTTTTCAATTTGGCAAGCTGCAAGAGCTTTGAGTAGGAGAGG 960
DB 901 TCAGCTGAATCATCTCTTTTCAATTTGGCAAGCTGCAAGAGCTTTGAGTAGGAGAGG 960
QY 961 AGTGCGCGGAGGCGGGGCGGGGCGGTGGAGCTGGGTGGCGGTGGCGGTGGCGGT 1020
DB 961 AGTGCGCGGAGGCGGGGCGGGGCGGTGGAGCTGGGTGGCGGTGGCGGTGGCGGT 1020
QY 1021 GGTGCGCGGAGGCGGGGCGGGGCGGTGGAGCTGGGTGGCGGTGGCGGTGGCGGT 1080
DB 1021 GGTGCGCGGAGGCGGGGCGGGGCGGTGGAGCTGGGTGGCGGTGGCGGTGGCGGT 1080
QY 1081 TTGTCCTCTCTGCTTGGCTTCTTTTCCAGCATTTTCCAGGATAACTGTGACTCCAG 1140
DB 1081 TTGTCCTCTCTGCTTGGCTTCTTTTCCAGCATTTTCCAGGATAACTGTGACTCCAG 1140
QY 1141 G 1141
DB 1141 G 1141
RESULT 2
AAS46482/c
ID AAS46482 standard; DNA; 12426 BP.
XX AAS46482;
AC AAS46482;
XX XX
DT 18-DEC-2001 (first entry)
XX Tumour suppressor gene derived chemically modified sequence #204.
XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
XX cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
XX cytosine methylation; ds.
XX Homo sapiens.
XX WO200168912-A2.
XX

XX DE Human cDNA clone (3'-primer) SEQ ID NO:10310.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-0116126.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 27-AUG-1999; 99JP-0300253.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PR 09-JUN-2000; 2000JP-0241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX PS Claim 3; SEQ ID 10310; 2537pp + CD ROM; English.
 XX CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX SQ Sequence 568 BP; 141 A; 148 C; 128 G; 142 T; 9 other;
 Query Match 17.1%; Score 195; DB 22; Length 568;
 Best Local Similarity 80.6%; Pred. No. 2.9e-43;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 177 TTTTGTCTCTGTCACCCAGGCTGAAGTACAGTGTAGCTCACGGCTCAGTGCAGCTTTGA 236
 DB 13 TCTTGTCTCTGTCACCCAGGCTGAAGTACAGTGTAGCTCACGGCTCAGTGCAGCTTTGA 72
 QY 237 CTTCCAGGCTCAAGTGAATCCTCTCGTCTCAGCTTTCCAGTAACCTGGGACCAAGGCAT 296
 DB 73 CTTCCAGGCTCAGGTGATCTCTCCACCTCCAGCTCCCGAGTAGTGGGACTACAGGCAT 132
 QY 297 GCATACACCGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCTCACCATTGG 356
 DB 133 GCACCAACCGCTCCAGCTAAATTTTGTACTTTTGTAGAGACGGGTTTCACCATGTTG 192

QY 357 CCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 416
 DB 193 CACAGGCTGGTCTCAGACTCTCTGGGCTCAAGCTATCCGCTTGGCTCCCAATG 252
 QY 417 CTGGGATTACAGGCTGAGCCACCGGCGGCGGCTGAGTAATC 459
 DB 253 CTGGGATTACAACTGGGAGCCACCGTGCCTCCGCGCCGAGATCTC 295
 RESULT 5
 AAH16727/c
 ID AAH16727 standard; cDNA; 2343 BP.
 XX AC AAH16727;
 XX DT 26-JUN-2001 (first entry)
 XX DE Human cDNA sequence SEQ ID NO:15908.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-0116126.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 27-AUG-1999; 99JP-0300253.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PR 09-JUN-2000; 2000JP-0241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX PS Claim 8; SEQ ID 15908; 2537pp + CD ROM; English.
 XX CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX CC

Tue Jun 10 08:56:17 2003

us-09-617-174c-1.rng

```
SQ      Sequence 2343 BP; 603 A; 515 C; 535 G; 690 T; 0 other;
Query Match      17.1%; Score 195; DB 22; Length 2343;
Best Local Similarity 80.8%; Pred. No. 5.5e-43;
Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY      177 TTTTGTCTGTCAACCAGGCTGAAGTACAGTGTAGTGTAGCTCAGGCTCACTGAGCTTTGA 236
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2331 TCTTGTCTGTCAACCAGGCTGAAGTACAGTGTAGTGTAGCTCAGGCTCACTGAGCTTTGA 2272

QY      237 CTTCCAGGCTCAAGTATCTCTCTCAGCTTTCAGTTCCTCCAGTAACTGGGACACAGGCAT 296
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2271 CTTCCAGGCTCAGTGTATCTCTCCACCTCAGGCTCCCGAGTACCTGGGACTACAGGCAT 2212

QY      297 GCATCACCAGCTAGGCTATTGTTTACATTTTTCAGATGAGGCTCTCACCATTGTG 356
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2211 GCACCCAGCTCAGCTATTTTGTACTTTTTCAGAGAGCGGGTTTCCACCATGTTG 2152

QY      357 CCCAGGTTGTCTCAAACTCCTGGGCTCAAGCAATCGGCTCAGTCAACTCCCAATG 416
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2151 CACAGGCTGTCTCAGACTCCTGGGCTCAAGCTATCGGCTATCGGCTCGGCTCCCAAGTG 2092

QY      417 CTGGGATTACAGGCTCAGCCAGCCGCGGCGGCTGAGTAATC 459
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2091 CTGGGATTACAACTGGGAGCCCGGTGCCCGGCCCGAGATCTC 2049

RESULT 6
ABK87050
ID      ABK87050 standard; cDNA; 66804 BP.
XX
AC      ABK87050;
XX
DT      07-OCT-2002 (first entry)
XX
DE      Human transporter protein genomic DNA.
XX
KW      Human; gene; ds; transporter protein; hTP; chromosome 12;
KW      Na-dependent inorganic phosphate co-transporter; cell proliferation;
KW      cell differentiation; cell signalling; gene therapy; protein therapy;
KW      antigen; vaccine; diagnosis; single nucleotide polymorphism; SNP.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Location/Qualifiers
FT      2029..2129
FT      exon
FT      /tag= a
FT      /number= 1
FT      2130..25338
FT      intron
FT      /tag= b
FT      /number= 1
FT      /cons_splice= (5'site:Yes,3'site:No)
FT      25339..25591
FT      exon
FT      /tag= c
FT      /number= 2
FT      25592..35639
FT      intron
FT      /tag= d
FT      /number= 2
FT      /cons_splice= (5'site:Yes,3'site:No)
FT      35640..35758
FT      exon
FT      /tag= e
FT      /number= 3
FT      35759..38007
FT      intron
FT      /tag= f
FT      /number= 3
FT      38008..38122
FT      exon
FT      /tag= g
FT      /number= 4
FT      38123..40966
FT      intron
FT      /tag= h
FT      /number= 4
FT      40967..41054
FT      exon
FT      /tag= i
```

```
FT      intron
FT      /number= 5
FT      41055..46414
FT      /tag= j
FT      /number= 5
FT      46415..46501
FT      exon
FT      /tag= k
FT      /number= 6
FT      46502..46977
FT      intron
FT      /tag= l
FT      /number= 6
FT      46978..47117
FT      exon
FT      /tag= m
FT      /number= 7
FT      47118..47233
FT      intron
FT      /tag= n
FT      /number= 7
FT      /cons_splice= (5'site:No,3'site:No)
FT      47234..47383
FT      exon
FT      /tag= o
FT      /number= 8
FT      47384..48675
FT      intron
FT      /tag= p
FT      /number= 8
FT      48676..48808
FT      exon
FT      /tag= q
FT      /number= 9
FT      48809..57401
FT      intron
FT      /tag= r
FT      /number= 9
FT      57402..57512
FT      exon
FT      /tag= s
FT      /number= 10
FT      57513..62660
FT      intron
FT      /tag= t
FT      /number= 10
FT      62661..62788
FT      exon
FT      /tag= u
FT      /number= 11
FT      62789..64446
FT      intron
FT      /tag= v
FT      /number= 11
FT      /cons_splice= (5'site:Yes,3'site:No)
FT      64447..64791
FT      exon
FT      /tag= w
FT      /number= 12
FT      replace(899,C)
FT      /tag= x
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(3052,T)
FT      /tag= y
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(4813,G)
FT      /tag= z
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(5882,T)
FT      /tag= aa
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(5962,C)
FT      /tag= ab
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(12831..12833,AG)
FT      /tag= ac
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(12833..12835,GC)
FT      /tag= ad
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(13561,C)
FT      /tag= ae
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(14023,T)
FT      /tag= af
FT      /standard_name= "Single nucleotide polymorphism"
FT      replace(14483..14485,AT)
```


PR	07-JUN-2000;	2000US-02094567.	XX
PR	28-JUN-2000;	2000US-0214986.	XX
PR	30-JUN-2000;	2000US-0215135.	XX
PR	07-JUL-2000;	2000US-0216647.	XX
PR	07-JUL-2000;	2000US-0216880.	XX
PR	11-JUL-2000;	2000US-0217487.	XX
PR	11-JUL-2000;	2000US-0217496.	XX
PR	14-JUL-2000;	2000US-0218290.	XX
PR	26-JUL-2000;	2000US-0220963.	XX
PR	26-JUL-2000;	2000US-0220964.	XX
PR	14-AUG-2000;	2000US-0224518.	XX
PR	14-AUG-2000;	2000US-0224519.	XX
PR	14-AUG-2000;	2000US-0225213.	XX
PR	14-AUG-2000;	2000US-0225214.	XX
PR	14-AUG-2000;	2000US-0225266.	XX
PR	14-AUG-2000;	2000US-0225267.	XX
PR	14-AUG-2000;	2000US-0225268.	XX
PR	14-AUG-2000;	2000US-0225270.	XX
PR	14-AUG-2000;	2000US-0225447.	XX
PR	14-AUG-2000;	2000US-0225757.	XX
PR	14-AUG-2000;	2000US-0225758.	XX
PR	14-AUG-2000;	2000US-0225759.	XX
PR	18-AUG-2000;	2000US-0226279.	XX
PR	22-AUG-2000;	2000US-0226681.	XX
PR	22-AUG-2000;	2000US-0226888.	XX
PR	22-AUG-2000;	2000US-0227182.	XX
PR	23-AUG-2000;	2000US-0227009.	XX
PR	30-AUG-2000;	2000US-0228924.	XX
PR	01-SEP-2000;	2000US-0229287.	XX
PR	01-SEP-2000;	2000US-0229343.	XX
PR	01-SEP-2000;	2000US-0229344.	XX
PR	01-SEP-2000;	2000US-0229345.	XX
PR	05-SEP-2000;	2000US-0229509.	XX
PR	05-SEP-2000;	2000US-0229513.	XX
PR	06-SEP-2000;	2000US-0230437.	XX
PR	06-SEP-2000;	2000US-0230438.	XX
PR	08-SEP-2000;	2000US-0231242.	XX
PR	08-SEP-2000;	2000US-0231243.	XX
PR	08-SEP-2000;	2000US-0231244.	XX
PR	08-SEP-2000;	2000US-0231413.	XX
PR	08-SEP-2000;	2000US-0231414.	XX
PR	08-SEP-2000;	2000US-0232080.	XX
PR	08-SEP-2000;	2000US-0232081.	XX
PR	12-SEP-2000;	2000US-0231968.	XX
PR	14-SEP-2000;	2000US-0232397.	XX
PR	14-SEP-2000;	2000US-0232398.	XX
PR	14-SEP-2000;	2000US-0232399.	XX
PR	14-SEP-2000;	2000US-0232400.	XX
PR	14-SEP-2000;	2000US-0232401.	XX
PR	14-SEP-2000;	2000US-0233063.	XX
PR	14-SEP-2000;	2000US-0233064.	XX
PR	14-SEP-2000;	2000US-0233065.	XX
PR	21-SEP-2000;	2000US-0234223.	XX
PR	21-SEP-2000;	2000US-0234274.	XX
PR	25-SEP-2000;	2000US-0234997.	XX
PR	25-SEP-2000;	2000US-0234998.	XX
PR	26-SEP-2000;	2000US-0235484.	XX
PR	27-SEP-2000;	2000US-0235634.	XX
PR	27-SEP-2000;	2000US-0235836.	XX
PR	29-SEP-2000;	2000US-0236327.	XX
PR	29-SEP-2000;	2000US-0236367.	XX
PR	29-SEP-2000;	2000US-0236368.	XX
PR	29-SEP-2000;	2000US-0236369.	XX
PR	29-SEP-2000;	2000US-0236370.	XX
PR	02-OCT-2000;	2000US-0236802.	XX
PR	02-OCT-2000;	2000US-0237037.	XX
PR	02-OCT-2000;	2000US-0237038.	XX
PR	02-OCT-2000;	2000US-0237039.	XX
PR	02-OCT-2000;	2000US-0237040.	XX
PR	13-OCT-2000;	2000US-0239935.	XX
PR	20-OCT-2000;	2000US-0240960.	XX
PR	20-OCT-2000;	2000US-0241221.	XX
PR	20-OCT-2000;	2000US-0241785.	XX
PR	20-OCT-2000;	2000US-0241786.	XX
PR	20-OCT-2000;	2000US-0241787.	XX
PR	20-OCT-2000;	2000US-0241808.	XX
PR	20-OCT-2000;	2000US-0241809.	XX
PR	20-OCT-2000;	2000US-0241826.	XX
PR	01-NOV-2000;	2000US-0244617.	XX
PR	08-NOV-2000;	2000US-0246474.	XX
PR	08-NOV-2000;	2000US-0246475.	XX
PR	08-NOV-2000;	2000US-0246	

PR	26-JUL-2000;	2000US-2000;	2000US-0220963;
PR	26-JUL-2000;	2000US-2000;	2000US-0220964;
PR	26-JUL-2000;	2000US-2000;	2000US-0220965;
PR	26-JUL-2000;	2000US-2000;	2000US-0220966;
PR	14-AUG-2000;	2000US-2000;	2000US-0224518;
PR	14-AUG-2000;	2000US-2000;	2000US-0224519;
PR	14-AUG-2000;	2000US-2000;	2000US-0224521;
PR	14-AUG-2000;	2000US-2000;	2000US-0225214;
PR	14-AUG-2000;	2000US-2000;	2000US-0225266;
PR	14-AUG-2000;	2000US-2000;	2000US-0225267;
PR	14-AUG-2000;	2000US-2000;	2000US-0225268;
PR	14-AUG-2000;	2000US-2000;	2000US-0225270;
PR	14-AUG-2000;	2000US-2000;	2000US-0225447;
PR	14-AUG-2000;	2000US-2000;	2000US-0225757;
PR	14-AUG-2000;	2000US-2000;	2000US-0225758;
PR	14-AUG-2000;	2000US-2000;	2000US-0225759;
PR	18-AUG-2000;	2000US-0226279;	2000US-0226279;
PR	22-AUG-2000;	2000US-0226681;	2000US-0226681;
PR	22-AUG-2000;	2000US-0226868;	2000US-0226868;
PR	22-AUG-2000;	2000US-0227182;	2000US-0227182;
PR	23-AUG-2000;	2000US-0227000;	2000US-0227000;
PR	23-AUG-2000;	2000US-0228924;	2000US-0228924;
PR	01-SEP-2000;	2000US-0229287;	2000US-0229287;
PR	01-SEP-2000;	2000US-0229343;	2000US-0229343;
PR	01-SEP-2000;	2000US-0229344;	2000US-0229344;
PR	01-SEP-2000;	2000US-0229345;	2000US-0229345;
PR	05-SEP-2000;	2000US-0229509;	2000US-0229509;
PR	05-SEP-2000;	2000US-0229513;	2000US-0229513;
PR	06-SEP-2000;	2000US-0230437;	2000US-0230437;
PR	06-SEP-2000;	2000US-0230438;	2000US-0230438;
PR	08-SEP-2000;	2000US-0231143;	2000US-0231143;
PR	08-SEP-2000;	2000US-0231144;	2000US-0231144;
PR	08-SEP-2000;	2000US-0232080;	2000US-0232080;
PR	08-SEP-2000;	2000US-0232081;	2000US-0232081;
PR	12-SEP-2000;	2000US-0231968;	2000US-0231968;
PR	14-SEP-2000;	2000US-0232197;	2000US-0232197;
PR	14-SEP-2000;	2000US-0233064;	2000US-0233064;
PR	14-SEP-2000;	2000US-0233065;	2000US-0233065;
PR	14-SEP-2000;	2000US-0232198;	2000US-0232198;
PR	14-SEP-2000;	2000US-0232199;	2000US-0232199;
PR	14-SEP-2000;	2000US-0232400;	2000US-0232400;
PR	14-SEP-2000;	2000US-0234031;	2000US-0234031;
PR	14-SEP-2000;	2000US-0233063;	2000US-0233063;
PR	14-SEP-2000;	2000US-0233064;	2000US-0233064;
PR	21-SEP-2000;	2000US-0234221;	2000US-0234221;
PR	21-SEP-2000;	2000US-0234274;	2000US-0234274;
PR	25-SEP-2000;	2000US-0234597;	2000US-0234597;
PR	25-SEP-2000;	2000US-0234598;	2000US-0234598;
PR	26-SEP-2000;	2000US-0235484;	2000US-0235484;
PR	27-SEP-2000;	2000US-0235634;	2000US-0235634;
PR	27-SEP-2000;	2000US-0235635;	2000US-0235635;
PR	29-SEP-2000;	2000US-0236327;	2000US-0236327;
PR	29-SEP-2000;	2000US-0236367;	2000US-0236367;
PR	29-SEP-2000;	2000US-0236368;	2000US-0236368;
PR	29-SEP-2000;	2000US-0236369;	2000US-0236369;
PR	29-SEP-2000;	2000US-0236370;	2000US-0236370;
PR	02-OCT-2000;	2000US-0236802;	2000US-0236802;
PR	02-OCT-2000;	2000US-0237037;	2000US-0237037;
PR	02-OCT-2000;	2000US-0237038;	2000US-0237038;
PR	02-OCT-2000;	2000US-0237039;	2000US-0237039;
PR	02-OCT-2000;	2000US-0237040;	2000US-0237040;
PR	13-OCT-2000;	2000US-0239935;	2000US-0239935;
PR	13-OCT-2000;	2000US-0239937;	2000US-0239937;
PR	20-OCT-2000;	2000US-0240860;	2000US-0240860;
PR	20-OCT-2000;	2000US-0241809;	2000US-0241809;
PR	20-OCT-2000;	2000US-0241826;	2000US-0241826;
PR	20-OCT-2000;	2000US-0242221;	2000US-0242221;
PR	01-NOV-2000;	2000US-0244617;	2000US-0244617;
PR	08-NOV-2000;	2000US-0246474;	2000US-0246474;

PR	08-NOV-2000;	2000US-0246475.
PR	08-NOV-2000;	2000US-0246476.
PR	08-NOV-2000;	2000US-0246477.
PR	08-NOV-2000;	2000US-0246478.
PR	08-NOV-2000;	2000US-0246479.
PR	08-NOV-2000;	2000US-0246523.
PR	08-NOV-2000;	2000US-0246524.
PR	08-NOV-2000;	2000US-0246525.
PR	08-NOV-2000;	2000US-0246526.
PR	08-NOV-2000;	2000US-0246527.
PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249244.
PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250391.
PR	01-DEC-2000;	2000US-0251160.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	06-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
XX	WPI; 2001-541565/60.	
DR		
XX		
PT	Nucleic acids encoding 3224 human nervous system antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating nervous system	
PT	cancers and metastases -	
XX		
PS	Disclosure; SEQ ID NO 12920; 1701pp + Sequence Listing; English.	
XX		
CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins	
CC	(ABBL4578-ABBL8001) useful for preventing, treating or ameliorating	
CC	medical conditions e.g. by protein or gene therapy. The genes are	
CC	isolated from a range of human tissues disclosed in the specification.	
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful	
CC	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast	
CC	and ovarian cancer and other cancers of the adrenal gland, bone, bone	
CC	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;	
CC	(b) immune disorders e.g. Addison's disease, allergies, autoimmune	
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's	
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative	
CC	colitis; (c) cardiovascular disorders such as myocardial ischaemias;	
CC	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and	

CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 32184 BP; 7866 A; 6152 C; 6798 G; 11368 T; 0 other;

Query Match 16.2%; Score 185.4; DB 22; Length 32184;
Best Local Similarity 74.3%; Pred. No. 7.7e-40;
Matches 234; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 137 TTTCAGAGCAGAGCTGGGTAAGTCTCTTTCTTTTGTCTTCTGTCAACCCAGGC 196
Db 2244 TTTGTTATTATGGTGTAATCTTTTTTTTTTGACAAAGATCTTGTCTTCTCCAGGC 2303

Qy 197 TGAAGTACAGTGGTTAGCTCACGGCTCACATGCGAGCTTTGACCTCCCAAGGCTCAAGTGATC 256
Db 2304 TGGAGTCAGTGGTATGATCTTGGCTCACATTCAGCCTTGAACCTCCAGGCTCAAGTGGTC 2363

Qy 257 CTCGCGTCTCAGCTTTCCAAAGTAAGTCTGGGACACAGCATGCATCACACGCTAGGCTAT 316
Db 2364 CTCCTGCTTCAGCCCCCAAGTAGTGGGACTACAGGAGTGGGCCACCATCTCTAGCTAA 2423

Qy 317 TGTTTTACATTTTTTTGTAGAGATGGGGTCTCACCATGTGCGCCAGTGTGGTCTCAAACTC 376
Db 2424 TTTTTTTTTTTTTTCTAGAGATTAGTCTCACCATGTGCGCCAGGCTGGTCTCAAACTC 2483

Qy 377 CTGGGCTCAAGCAATCGCTCACGTCACCTCCCAATGCTGGGATTCAGGCGTGAGC 436
Db 2484 CTGGGCTCAAGCAATCTCTCTGCTTGGCCCTCCCAAGTTCCTGGATTACAGATGTGAGC 2543

Qy 437 CACCGGGCCAGGGCT 451
Db 2544 CACTACCCCTGGCCT 2558

RESULT 9
ABA20590
ID ABA20590 standard, DNA; 32184 BP.
XX
AC ABA20590;
XX
DT
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 12921.
XX Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparasitic; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebrotropic; antineuroinflammatory;
KW antiallergic; antidiabetic; antilucer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220363.
PR 26-JUL-2000; 2000US-0220364.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226581.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231568.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234374.
PR 25-SEP-2000; 2000US-0234397.
PR 25-SEP-2000; 2000US-0234398.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237017.
PR 02-OCT-2000; 2000US-0237017.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.

PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249318.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251656.
PR 08-DEC-2000; 2000US-0251668.
PR 08-DEC-2000; 2000US-0251669.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2000US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 324 human nervous system antigen polypeptides,
useful for preventing, diagnosing and/or treating nervous system
cancers and metastases -

Disclosure; SEQ ID NO 12921; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins
(ABP14678-ABP18001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (ant)agonists are useful
in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
and ovarian cancer and other cancers of the adrenal gland, bone, bone

PR	28-JUN-2000;	2000US-0214886;
PR	30-JUN-2000;	2000US-0215135;
PR	07-JUL-2000;	2000US-0216647;
PR	10-JUL-2000;	2000US-0216880;
PR	11-JUL-2000;	2000US-0217486;
PR	11-JUL-2000;	2000US-0218290;
PR	14-JUL-2000;	2000US-0220963;
PR	26-JUL-2000;	2000US-0220964;
PR	26-JUL-2000;	2000US-0220964;
PR	14-AUG-2000;	2000US-0224518;
PR	14-AUG-2000;	2000US-0224519;
PR	14-AUG-2000;	2000US-0225213;
PR	14-AUG-2000;	2000US-0225214;
PR	14-AUG-2000;	2000US-0225266;
PR	14-AUG-2000;	2000US-0225267;
PR	14-AUG-2000;	2000US-0225268;
PR	14-AUG-2000;	2000US-0225270;
PR	14-AUG-2000;	2000US-0225447;
PR	14-AUG-2000;	2000US-0225757;
PR	14-AUG-2000;	2000US-0225758;
PR	14-AUG-2000;	2000US-0225759;
PR	18-AUG-2000;	2000US-0226279;
PR	22-AUG-2000;	2000US-0226681;
PR	22-AUG-2000;	2000US-0228686;
PR	22-AUG-2000;	2000US-0227182;
PR	23-AUG-2000;	2000US-0227009;
PR	30-SEP-2000;	2000US-0228924;
PR	01-SEP-2000;	2000US-0229287;
PR	01-SEP-2000;	2000US-0229343;
PR	01-SEP-2000;	2000US-0229344;
PR	01-SEP-2000;	2000US-0229345;
PR	05-SEP-2000;	2000US-0229509;
PR	05-SEP-2000;	2000US-0229513;
PR	06-SEP-2000;	2000US-0230437;
PR	06-SEP-2000;	2000US-0230438;
PR	08-SEP-2000;	2000US-0231242;
PR	08-SEP-2000;	2000US-0231243;
PR	08-SEP-2000;	2000US-0231244;
PR	08-SEP-2000;	2000US-0231413;
PR	08-SEP-2000;	2000US-0231414;
PR	08-SEP-2000;	2000US-0232080;
PR	08-SEP-2000;	2000US-0232081;
PR	12-SEP-2000;	2000US-0231968;
PR	14-SEP-2000;	2000US-0232397;
PR	14-SEP-2000;	2000US-0232398;
PR	14-SEP-2000;	2000US-0232399;
PR	14-SEP-2000;	2000US-0232400;
PR	14-SEP-2000;	2000US-0232401;
PR	14-SEP-2000;	2000US-0233063;
PR	14-SEP-2000;	2000US-0233064;
PR	14-SEP-2000;	2000US-0233065;
PR	21-SEP-2000;	2000US-0234223;
PR	21-SEP-2000;	2000US-0234274;
PR	21-SEP-2000;	2000US-0234997;
PR	25-SEP-2000;	2000US-0235498;
PR	26-SEP-2000;	2000US-0235484;
PR	27-SEP-2000;	2000US-0235834;
PR	27-SEP-2000;	2000US-0235836;
PR	29-SEP-2000;	2000US-0236327;
PR	29-SEP-2000;	2000US-0236367;
PR	29-SEP-2000;	2000US-0236368;
PR	29-SEP-2000;	2000US-0236369;
PR	29-SEP-2000;	2000US-0236370;
PR	02-OCT-2000;	2000US-0236802;
PR	02-OCT-2000;	2000US-0237037;
PR	02-OCT-2000;	2000US-0237038;
PR	02-OCT-2000;	2000US-0237039;
PR	02-OCT-2000;	2000US-0237040;
PR	13-OCT-2000;	2000US-0235935;
PR	13-OCT-2000;	2000US-0235937;
PR	20-OCT-2000;	2000US-0240960;
PR	20-OCT-2000;	2000US-0241221;
PR	20-OCT-2000;	2000US-0241785;

PR	20-OCT-2000;	2000US-0241786;
PR	20-OCT-2000;	2000US-0241787;
PR	20-OCT-2000;	2000US-0241808;
PR	20-OCT-2000;	2000US-0241809;
PR	20-OCT-2000;	2000US-0241826;
PR	01-NOV-2000;	2000US-0246171;
PR	08-NOV-2000;	2000US-02464617;
PR	08-NOV-2000;	2000US-0246475;
PR	08-NOV-2000;	2000US-0246476;
PR	08-NOV-2000;	2000US-0246477;
PR	08-NOV-2000;	2000US-0246478;
PR	08-NOV-2000;	2000US-0246523;
PR	08-NOV-2000;	2000US-0246524;
PR	08-NOV-2000;	2000US-0246525;
PR	08-NOV-2000;	2000US-0246526;
PR	08-NOV-2000;	2000US-0246527;
PR	08-NOV-2000;	2000US-0246528;
PR	08-NOV-2000;	2000US-0246532;
PR	08-NOV-2000;	2000US-0246509;
PR	08-NOV-2000;	2000US-0246610;
PR	08-NOV-2000;	2000US-0246611;
PR	08-NOV-2000;	2000US-0246613;
PR	17-NOV-2000;	2000US-0249207;
PR	17-NOV-2000;	2000US-0249208;
PR	17-NOV-2000;	2000US-0249209;
PR	17-NOV-2000;	2000US-0249210;
PR	17-NOV-2000;	2000US-0249211;
PR	17-NOV-2000;	2000US-0249212;
PR	17-NOV-2000;	2000US-0249213;
PR	17-NOV-2000;	2000US-0249214;
PR	17-NOV-2000;	2000US-0249215;
PR	17-NOV-2000;	2000US-0249216;
PR	17-NOV-2000;	2000US-0249217;
PR	17-NOV-2000;	2000US-0249218;
PR	17-NOV-2000;	2000US-0249244;
PR	17-NOV-2000;	2000US-0249245;
PR	17-NOV-2000;	2000US-0249264;
PR	17-NOV-2000;	2000US-0249265;
PR	17-NOV-2000;	2000US-0249297;
PR	17-NOV-2000;	2000US-0249299;
PR	17-NOV-2000;	2000US-0249300;
PR	01-DEC-2000;	2000US-0250160;
PR	01-DEC-2000;	2000US-0250391;
PR	05-DEC-2000;	2000US-0251030;
PR	05-DEC-2000;	2000US-0251988;
PR	06-DEC-2000;	2000US-0256719;
PR	08-DEC-2000;	2000US-0251479;
PR	08-DEC-2000;	2000US-0251856;
PR	08-DEC-2000;	2000US-0251869;
PR	08-DEC-2000;	2000US-0251989;
PR	08-DEC-2000;	2000US-0251990;
PR	11-DEC-2000;	2000US-0254097;
PR	05-JAN-2001;	2000US-0259678;

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased


```
FT      /*tag= ak
FT      /note= "binds probe"
FT      replace(39944,T)
FT      /tag= al
FT      complement(39945..39963)
FT      /tag= am
FT      39953..39970
FT      /tag= an
FT      39954..39972
FT      /tag= ao
FT      39961..39985
FT      /tag= ap
FT      /note= "binds probe"
FT      /tag= aq
FT      complement(39974..39992)
FT      /tag= ar
FT      40242..40259
FT      /tag= as
FT      41137..41154
FT      /tag= at
FT      41366..41384
FT      /tag= au
FT      41373..71397
FT      /tag= av
FT      /note= "binds probe"
FT      replace(41385,C)
FT      /tag= aw
FT      41385..41403
FT      /tag= ax
FT      complement(41386..41404)
FT      /tag= ay
FT      41392..41416
FT      /tag= az
FT      /note= "binds probe"
FT      replace(41404,C)
FT      /tag= ba
FT      complement(41405..41423)
FT      /tag= bb
FT      41564..41581
FT      /tag= bc
FT      42122..42141
FT      /tag= bd
FT      42213..42231
FT      /tag= be
FT      42220..42244
FT      /tag= bf
FT      /note= "binds probe"
FT      replace(42232,C)
FT      /tag= bg
FT      complement(42233..42251)
FT      /tag= bh
FT      42526..42543
FT      /tag= bi
FT      50436..50545
FT      /tag= bj
FT      /label= "G"
FT      67289..67309
FT      /tag= bk
FT      67456..67474
FT      /tag= bl
FT      67463..67487
FT      /tag= bm
FT      /note= "binds probe"
FT      replace(67475,G)
FT      /tag= bn
FT      complement(67476..67494)
FT      /tag= bo
FT      67724..67741
FT      /tag= bp
FT      69182..69200
FT      /tag= bq
FT      69502..69520
```

```
FT      /*tag= br
FT      69509..69533
FT      /tag= bs
FT      /note= "binds probe"
FT      replace(69521,G)
FT      /tag= bt
FT      complement(69522..69540)
FT      /tag= bu
FT      69609..69626
FT      /tag= bv
FT      72698..72715
FT      /tag= bw
FT      72819..72837
FT      /tag= bx
FT      72826..72850
FT      /tag= by
FT      /note= "binds probe"
FT      replace(72838,T)
FT      /tag= bz
FT      complement(72839..72857)
FT      /tag= ca
FT      72881..72918
FT      /tag= cb
FT      /label= "H"
FT      73099..73117
FT      /tag= cc

Query Match      16.2%; Score 184.6; DB 22; Length 240825;
Best Local Similarity 77.7%; Pred. No. 3.2e-39;
Matches 223; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY      161 TTTTCTTTTCTTTCTCTGTCTCACCAGGCTGAAGTACAGTGTAGTCTCAGG 220
      |||||
Db      230872 TTTTCTTTTCTTTCTCTGTCTCACCAGGCTGAAGTACAGTGTAGTCTCAGG 220
      |||||

QY      221 CTCACGTGAGTTTGCCTCCAGGCTCAAGTGATCTCTGTCTCAGCTTCCAGTAA 280
      |||||
Db      230812 CTCACGTGAACTCTACCTCCAGGCTCAAGCGATTCCCTCCAGCTCCCAAGTAG 230753
      |||||

QY      281 CTGGGACACAGGCGATGCATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
      |||||
Db      230752 CTGGGACTACATGCATGTGCCATCAGCCGGCTAATTTTGTATTTTGTAGAGATG 230693
      |||||

QY      341 GGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCGTGGGCTCAAGCAATCCGCTCAG 400
      |||||
Db      230692 GGGTTTGGCATGTTGGCCAGGCTGGTGTGAACCTCTGGCTCAAGCGATCTGCCGCC 230633
      |||||

QY      401 TCAACTCCCAATGCTGGGATTACAGGCGTGAGCCACCGGCCAG 447
      |||||
Db      230632 TTGGCCTCCAAAGTGTGGGATTACAGGCGTGAGCCACCGGCCCTG 230586
      |||||

RESULT 13
AAC79682/C
ID      AAC79682 standard; cDNA; 1162 BP.
XX
XX      AAC79682;
XX
XX      12-FEB-2001 (first entry)
XX
XX      Human secreted protein gene 2 SEQ ID NO:12.
XX
XX      Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
XX      nototropic; neuroprotective; antiviral; antiallergic; hepatotropic;
XX      antidiabetic; antiinflammatory; antitumor; antiparasitic; anticonvulsant;
XX      antibacterial; antifungal; antiparasitic; antitumor; antiparasitic;
XX      food additive; preservative; chromosome identification; cancer;
XX      immune disorder; cardiovascular disorder; neurological disease;
XX      wound healing; infectious disease; ss.
XX
XX      Homo sapiens.
XX
XX      WO200058339-A2.
FN
```

```
XX 05-OCT-2000.
XX
XX 22-MAR-2000; 2000WO-US07440.
XX
XX 26-MAR-1999; 99US-0126503.
XX 17-DEC-1999; 99US-0172409.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Komatsoulis G;
XX
XX WPI; 2000-594637/56.
XX P-PSDB; AAB44597.
XX
XX Fifty nucleic acid molecules encoding human secreted proteins, useful
XX in the prevention, treatment and diagnosis of cancer, immune disorders,
XX cardiovascular disorders and neurological diseases -
XX
XX Claim 1; Page 338; 410pp; English.
XX
XX The polynucleotide sequences given in AAC79681 to AAC79730 encode the
XX human secreted proteins given in AAB44596 to AAB44645. AAB44646 to
XX AAB44693 represent human secreted polypeptide sequences and proteins
XX homologous to them, which are given in the exemplification of the present
XX invention. Human secreted proteins have activities based on the tissues
XX and cells the genes are expressed in. Examples of activities include:
XX cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;
XX anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
XX antitumor; anticonvulsant; antibacterial; antifungal; antiparasitic; and
XX cardiant. The polynucleotides and polypeptides are useful for preventing,
XX treating or ameliorating a medical condition in e.g. humans, mice,
XX rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides
XX can also be used as a food additive or preservative to increase or
XX decrease storage capabilities. The polynucleotides are useful for
XX chromosome identification. They are also useful as probes for diagnosing
XX a disorder related to the female reproductive system, particularly breast
XX and/or ovarian cancer. They are also useful in the gene therapy of breast
XX and ovarian cancer. The nucleic acids, protein, antibodies, agonists and
XX antagonists from the present invention are useful in the diagnosis,
XX treatment and prevention of: cancer; immune disorders; cardiovascular
XX disorders; wound healing; neurological diseases; and infectious
XX diseases. AAC79672 to AAC79680 and AAB44595 represent sequences used in
XX the exemplification of the present invention.
XX
XX Sequence 1162 BP; 336 A; 218 C; 300 G; 308 T; 0 other;
XX
Query Match 16.1%; Score 184; DB 21; Length 1162;
Best Local Similarity 75.3%; Pred. No. 4.1e-40;
Matches 229; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 161 TTTTCTTTTGTCTTTTGTCTCTGTCACCCAGGCTGAAGTACAGTGGTTAGCTCACGG 220
DB 1153 TTTTCTTTTGTAGTCAGGATCTCTGTCACCTAGGTTGGAGTCAGTGGTCCATCATTA 1094
QY 221 CTCACGTGACGCTTGACCTCCAGGCTCAAGTGATCTCTGCTCTCAGCTTTTCCAAAGTAA 280
DB 1093 TTCAATGACGCTCAACCTCCACGCTCAAGTGATCTCTCCACCTCAACCTCCGAGCAG 1034
QY 281 CTGGGACCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 340
DB 1033 CTGGGACTACAGTGGCTCCACGAGCTGGTAAATTTTGTATTTTGTAGAGATG 974
QY 341 GGGTCTCACATGTTGCCAGGTTGCTCTCAACTCTGGCTCAAGCATCCGCTCAGC 400
DB 973 GGGTCTTACATGTTGCCAGGCTGGTCTCGAATCTCTGGGCTCAAGTATCTCCACC 914
QY 401 TCAACCTCCCAATGCTGGGATTTACAGGCTGAGCCAGCCGCGGCTGAGTATATCC 460
DB 913 TCTGTCTCCCAAGTGTGGGATTTACAGGATGAGCCAGCCAGCCGCGGCAATTTTCT 854
QY 461 TAAT 464
|||
```

```
DB 853 TATT 850
RESULT 14
AAL05557
ID AAL05557 standard; DNA; 735 BP.
XX
XX AAL05557;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human reproductive system related antigen DNA SEQ ID NO: 8245.
XX
XX Human reproductive system related antigen; reproductive system disorder;
XX cancer; gene therapy; ds.
XX
XX Homo sapiens.
XX
XX WO200155320-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01339.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180528.
XX 24-FEB-2000; 2000US-0184564.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189374.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205315.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226686.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
```

Tue Jun 10 08:56:17 2003

PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 14-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 21-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 25-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.

PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; SEQ ID NO 8245; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX SQ Sequence 735 BP; 191 A; 174 C; 166 G; 204 T; 0 other;
Query Match 16.1%; Score 183.4; DB 22; Length 735;
Best Local Similarity 78.3%; Pred. No. 4.8e-40;
Matches 220; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 177 TTTTGTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGCTCAGGCTCAGTGGCTTTGA 236
Db 249 TCTCCACGTGTACCCAGGCTAGTGTGAGTGGTAAATCAACATCACTCAGCCTTTGA 308
QY 237 CTTCCAGGCTCAAGTGAATCTCTGCTCAGCTTCCAGTAACTGGGACACAGGCAT 296
Db 309 CTTCTGGGCTCAGGTGATCTCTGCTCAGCTTCCAGCTCCTCAGGAGCTGGATTTAGGCT 368
QY 297 GCATCACCAGCTAGGCTATTGTTTACATTTTTTTAGAGATGGGCTCACCATTGTTG 356
Db 369 GTGCCAACATGTCAGGCTAATTTTTTTGATTTTGTAGAGATGGGCTCACCATTGCTG 428
QY 357 CCCAGGTTGGTCTCAAACTCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAATG 416
Db 429 CGCAGGCTGGTCTCAAACTCCTGGACTCAAGCAATCTCCACCTCAGCCTCCCAATG 488
QY 417 CTGGATTACAGCGTGAGCCACCGGCGGAGCTGAGTAA 457
Db 489 CTGGATTACAGCGTGAGCCACTGTGCCCAAGTAA 529

RESULT 15

AAK89703
ID AAK89703 standard; DNA; 735 BP.

XX
XX AAK89703;
XX AC

XX 05-NOV-2001 (first entry)

XX Human digestive system antigen genomic sequence SEQ ID NO: 3279.

XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
XX ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX digestive system disorder; Meckel's diverticulum; ds.

XX

OS Homo sapiens.
XX WO200155314-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US011324.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220363.
PR 26-JUL-2000; 2000US-0220364.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225271.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-02311242.
PR 08-SEP-2000; 2000US-02311243.
PR 08-SEP-2000; 2000US-02311244.
PR 08-SEP-2000; 2000US-0231143.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241308.
PR 20-OCT-2000; 2000US-0241309.
PR 20-OCT-2000; 2000US-0241326.
PR 01-NOV-2000; 2000US-0244517.
PR 08-NOV-2000; 2000US-0245474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI. INC.

Tue Jun 10 08:56:17 2003

XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-502630/55.
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases -
XX
PT
XX Disclosure; SEQ ID NO 3279; 986pp; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention.
XX
SQ Sequence 735 BP; 191 A; 174 C; 166 G; 204 T; 0 other;

Query Match 16.1%; Score 183.4; DB 22; Length 735;
Best Local Similarity 78.3%; Pred. No. 4.8e-40;
Matches 220; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 177 TTTTGTCTCTACCCAGGCTGAAGTACAGTGTAGCTCAGGCTCAGTGCAGCTTTGA 236
Db |||||
249 TCTCCCACTGTACCCAGGCTAGTGTGACAGTCAATCACAACCTCAGTGCAGCTTTGA 308
Qy 237 CCTCCAGGCTCAAGTATCTCTCGTCTCAGCTTTCCAAAGTAACTGGGACCAAGGCAT 296
Db |||||
309 CTTCCTGGGCTCAGGTATCTCTCGCTCAGCTCTGAGGAGCTGGGATTATAGCGT 368
Qy 297 GCATCACACGCTAGGCTATTGTTTACATTTTGTAGAGATGGGTCTCACCATGTTG 356
Db |||||
369 GTGCCAACATGTCAGGCTAATTTTGTATTTTGTAGAGATGGGTCTCACCATGCTG 428
Qy 357 CCCAGGTGCTCAAACTCTGGGCTCAAGCATCCGCTCAGTCAACCTCCCCAAATG 416
Db |||||
429 CGCAGGTGGTCTCAAACTCTGGACTCAAGCAATCTCCCACTCAGCCTCCCAATG 488
Qy 417 CTGGGATTACAGGCTGAGCCACCGGGCCAGGGCTGAGTAA 457
Db |||||
489 CTGGGATTAGAGGCTGAGCCACTGTGCCAGCCCAAGTAA 529

Search completed: June 7, 2003, 21:08:52
Job time : 442 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 21:08:57 ; Search time 83 Seconds
(without alignments)
4215.882 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagagagag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 153338391 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.Listing first 45 summaries

Database :

- Issued Patents NA:**
1: /cgn2_6/prodata/2/ina/5A COMB.seq**
2: /cgn2_6/prodata/2/ina/5B COMB.seq**
3: /cgn2_6/prodata/2/ina/6A COMB.seq**
4: /cgn2_6/prodata/2/ina/6B COMB.seq**
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq**
6: /cgn2_6/prodata/2/ina/backfile1.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	179.8	15.8	35060	3	US-08-814-095-7
2	178.6	15.7	70000	4	US-09-851-896-3
3	175.8	15.4	36741	4	US-09-301-665-3
4	174.4	15.3	40000	4	US-09-780-049-18
5	173	15.2	1988	2	US-08-257-963B-11
6	173	15.2	1988	4	US-08-367-841A-11
7	173	15.2	1988	5	PCT-US95-07201-11
8	173	15.2	5262	4	US-08-520-373D-5
9	173	15.2	22481	4	US-08-367-841A-43
10	173	15.2	22481	5	PCT-US95-07201-43
11	173	15.2	22484	4	US-09-875-223-2
12	173	15.2	99500	4	US-09-798-096-10
13	172.6	15.1	4421	2	US-08-257-963B-9
14	172.6	15.1	4421	4	US-08-367-841A-9
15	172.6	15.1	4421	4	US-08-520-373D-6
16	172.6	15.1	4421	5	PCT-US95-07201-9
17	172	15.1	3881	4	US-09-333-593A-1
18	171.8	15.1	81001	4	US-09-750-580-1
19	171.6	15.0	14747	4	US-09-608-285A-42
20	170.8	15.0	15977	4	US-09-608-285A-59
21	170	14.9	246240	2	US-08-724-394A-20
22	170	14.9	246240	2	US-08-724-394A-21
23	170	14.9	246240	2	US-08-724-394A-22
24	169.6	14.9	4285	4	US-09-040-774-1
C 25	169.4	14.8	1600	2	US-08-487-113D-117
C 26	169.4	14.8	1600	2	US-08-720-420A-117
27	169	14.8	168575	4	US-09-426-290-1

28	168.6	14.8	20674	4	US-09-641-638-651	Sequence 651, App
C 29	168.6	14.8	43950	4	US-09-735-934A-3	Sequence 3, Appli
30	168.6	14.8	111282	4	US-09-754-250-3	Sequence 3, Appli
C 31	168.2	14.7	685	4	US-09-227-357-100	Sequence 10, App
C 32	168	14.7	12597	4	US-09-705-299-12	Sequence 12, Appl
C 33	168	14.7	98844	4	US-09-791-211-10	Sequence 10, Appl
C 34	167.8	14.7	112132	4	US-09-741-150-3	Sequence 3, Appli
C 35	167.4	14.7	2477	1	US-08-429-742-1	Sequence 1, Appli
C 36	167.4	14.7	112132	4	US-09-741-150-3	Sequence 3, Appli
37	167	14.6	80246	4	US-09-078-294-4	Sequence 4, Appli
38	167	14.6	80595	4	US-09-078-294-3	Sequence 3, Appli
C 39	166.8	14.6	1460	4	US-09-257-179-23	Sequence 23, Appl
40	166	14.5	72604	4	US-09-268-992-7	Sequence 7, Appli
41	166	14.5	72604	4	US-09-657-474-7	Sequence 7, Appli
C 42	165.8	14.5	70000	4	US-09-851-896-3	Sequence 3, Appli
C 43	165.8	14.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 44	165.8	14.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 45	165.8	14.5	246240	2	US-08-724-394A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHS"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:

```

/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 4
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (33297..33408)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 5
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (32959..33094)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 6
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (32569..32628)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 7
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (32386..32468)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 8
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (31894..32080)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 9
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (31363..31534)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 10
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (31131..31284)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 11
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (30816..31011)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 12
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (30470..30626)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 13
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (30187..30274)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 14
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (29945..30073)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 15
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (29664..29856)
/ OTHER INFORMATION: /gene= "ARS"
/ OTHER INFORMATION: /number= 16
/ US-08-814-095-7

```

	Query Match	15.8%; Score 179.8; DB 3; Length 35060;
	Best Local Similarity	72.6%; Presd. No. 4.le-41;
	Matches :246; Conservative	0; Mismatches 92; Indels 1; Gaps 1:
QY	145 CAGAGCTGCGTACTCCTTTTCCTTTTTGTTCCTCTGCTACCCAGGCTGAAGTAC	204
Dd	8393 CAATATCTATTTTTCTCTTTTAAGGGACAGGGFTTGCTCTGTCAACCAGGCTGTAGTAC	833
OY	205 AGTGGTAGCTCACGGGCTACTGCAGCTTTGACCTCCCAGGGTCAAAGTGANCTCTCTGTC	264

Matches 250; Conservative 0; Mismatches 115; Indels 1; Gaps 1;
Qy 98 TGGAGACAGGAGGACAAAGAACAGAGCTCCACGAAGAGATTTTCAGAGCAGAGCTGGGTAC 157
Db 489 TGGTTTCACAGGGGAATATACAGCTCTACAGATAGTCTTTTTTTTTTTTTTTTTTTTT 548
Qy 158 TCCTTTTTTTTTTTTTTTTTTTTTTCTCTGTGTACCCAGGCTGAAGTACAGTGGTTAGCTCA 217
Db 549 TNNCTTTCTGAGAGGAGTCTCGCTTTGTTCNCAGGCTGGAGTGCAGTGGTGTGATCT 608
Qy 218 CGGCTCATCTGAGCTTTGAGCTCTCCAGGCTCAAGTATCTCTCTCTCTCTCTCTCTCT 277
Db 609 CAGCTCATCTGCAACT 668
Qy 278 TAACTGGGACACAGGAGCATGCATCACCGCTAGGCTATTGTTTTTTCATTTTTTGTAGAG 337
Db 669 TAGCTGGGATTACAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 727
Qy 338 ATGGGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTCTGGGCTCAAGCAATCCGCTC 397
Db 728 ACGGGTTTTCACCATGTTGCTTAGGCTGGTCTCAAACTCTCTGGGCTCAAGCGATCCACCC 787
Qy 398 ACGTCAACCTCCCAATGCTGGGATTACAGGCTGAGCCACCGGCGCAGGCTGAGTAA 457
Db 788 GCCTTGGCTCCCAAGTGTGGGATTACAGGCTGAGCCACCGGCGCAGGCTGAGTAA 847
Qy 458 TCCTAA 463
Db 848 TCTTAA 853

RESULT 6
US-08-367-841A-11
; Sequence 11, Application US/08367841A
; Patent No. 6319687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA: 07/952,796
; APPLICATION NUMBER:
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 11:

Db 20204 CCTCCCAAGTTTAAGCAATTCCTGCTCAGCCTCCCAAGTAGCTGGTACTACAGTCTAT 20263
Qy 297 GCATCACCACGCTAGCTATTGTTTATACATTTTTTTGTAGAGATGGGTCTCAACCAATGTTG 356
Db 20264 GCACCAACATGCTAGCTAGTATTTTTTTTATTATTAGTGAGATGGGTTCACCATGATG 20323
Qy 357 CCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAATG 416
Db 20324 GCAGGCTGGCTCAAACTCTGACCTCAAGTATGCGGCCACCTTGGCCTCCCAAGT 20383
Qy 417 CTGGGATTACAGCGTGAGCCACCGGGCCAGG 448
Db 20384 CTGGGATTACAGGTGTGAGCCACCGGCTGG 20415

RESULT 5
US-08-257-963B-11
; Sequence 11, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, S.
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
; TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,963B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 751-6800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1988 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Human
; FEATURE:
; NAME/KEY: J1108
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: 2 kb PCR product using
; OTHER INFORMATION: primers, SEQ ID: 13 and 14.
US-08-257-963B-11
Query Match 15.2%; Score 173; DB 2; Length 1988;
Best Local Similarity 68.3%; Pred. No. 7.6e-40;

Tue Jun 10 08:56:18 2003

```
; Sequence 5, Application US/08520373D
; Patent No. 6451763
; GENERAL INFORMATION:
; APPLICANT: Tombran-Tink, Joyce
; APPLICANT: Steele, Fintan R
; APPLICANT: Chader, Gerald J
; APPLICANT: Becerra, Sofia P
; APPLICANT: Johnson, Lincoln V
; APPLICANT: Rodriguez, Ignacio R
; TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
; FILE REFERENCE: 2026-4203US1
; CURRENT APPLICATION NUMBER: US/08/520,373D
; CURRENT FILING DATE: 1995-08-29
; PRIOR APPLICATION NUMBER: 08/377,710
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/279,979
; PRIOR FILING DATE: 1994-07-25
; PRIOR APPLICATION NUMBER: 07/894,215
; PRIOR FILING DATE: 1992-06-04
; PRIOR APPLICATION NUMBER: 07/952,796
; PRIOR FILING DATE: 1992-09-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187;
; OTHER INFORMATION: EXON 5170-5255; INTRON 162-1141; INTRON
; OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS
; OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
; NAME/KEY: exon
; LOCATION: (35)..(160)
; NAME/KEY: exon
; LOCATION: (1142)..(1297)
; NAME/KEY: exon
; LOCATION: (1984)..(2187)
; NAME/KEY: exon
; LOCATION: (5170)..(5256)
; NAME/KEY: intron
; LOCATION: (162)..(1141)
; NAME/KEY: intron
; LOCATION: (1298)..(1983)
; NAME/KEY: intron
; LOCATION: (2188)..(5169)
; OTHER INFORMATION: n = a or g or t or c, any base
US-08-520-373D-5

Query Match 15.2%; Score 173; DB 4; Length 5262;
Best Local Similarity 68.3%; Pred. No. 1.3e-39;
Matches 250; Conservative 0; Mismatches 115; Indels 1; Gaps 1;

QY 98 TGGGAAGACAGGAGGACAGGCTCCACGAGGATTCAGAGCAGAGCTGCGTAC 157
DB 521 TGGGTTACAGGGGAACTAATACAGCTCCTACAGATAGTCTTTTTTTTTTTT 580
QY 158 TCCTTTTCTTTTCTTTTCTGCTGTGCTCACCAGCTCAAGTACAGTGTAGCTCA 217
DB 581 TNNCTTTCTGAGACGGAGTCTCGCTTTGTCCAAAGCTGGAGTGGTGTGTCT 640
QY 218 CGGCTCACTGGAGCTTTGACCTCCAGGCTCAAGTGTCTCTGCTCAGCTTTCCAAG 277
DB 641 CAGCTCACTGCAACTCTGCTCCCTCTGCTTCAAGGAATCTCTGCTCAGCTCCAG 700
QY 278 TAACTGGGACCAAGGATGATACACAGCTAGCTATGTTTACATTTTGTAGAG 337
DB 701 TAGCTGGGATTCAGGACCTGCCATCATGCCAGCTAAT-TTTTGTATTTTAGTAG 759
QY 338 ATGGGGTCTCACCATTGTTGCCAGGTTGGTCTCTCAACTCTGGGCTCAAGCAATCCGCTC 397
DB 760 ACGGGGTTTACCATTGTTGGCTTAGGCTGTCTCAAAACTCCCGGGCTCAAGCAATCCACC 819

; Sequence 43, Application US/08367841A
; Patent No. 6319687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22481 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: P1-147
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: full length genomic
; OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43

Query Match 15.2%; Score 173; DB 4; Length 22481;
Best Local Similarity 68.3%; Pred. No. 2.9e-39;
Matches 250; Conservative 0; Mismatches 115; Indels 1; Gaps 1;

QY 98 TGGGAACACAGGAGGACAGGCTCCACGAGGATTCAGAGCAGAGTTCAGAGCAGCTGCGTAC 157
DB 15086 TGGGTTCCAGGGGAACTAATACAGCTCCTACAGATAGTCTTTTTTTTTTTTTTTT 15145
```


401 TC AACCTTCCCAATGCTGGATTACAGGCGTAGCCACCGGGCCAGGCTGA 453

RESULT 13

US-08-257-963B-9
Sequence 9, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHA
TITLE OF INVENTION: BIOLOGICAL ACTIVITY A
TITLE OF INVENTION: AND EXPRESSING THE PR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4421 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Human
FEATURE:
NAME/KEY: JT101
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 7.1 kb Bam HI
OTHER INFORMATION: fragment Derived fr
OTHER INFORMATION: genomic DNA

US-08-257-963B-9

	Query Match	15.1%	Score 172.6;	DB 2;	Length 4421;
	Best Local Similarity	69.3%;	Pred. No. 1.5e-39;		
	Matches 235;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
149	QY	GCTGGTACTCCTTTTCTTTTCTTTTGTCTCTGTCA	CCCCAGGCTGAAGTACAGTG	208	
3788	Db	GCCTCTATTTTTTTTTTGTAGATGGAGTCTCACACTGTCACTGGGCTGGAGTGCAGTG	3847		
209	QY	GTTAGCTACGGCTCACTGCAGCTTTGACCTCCAGGGCTCAAGTGATCCTCTCGTCTCAG	268		
3848	Db	SAGCGATCTCGGCTCACTGCACACCTCCGGCTCCTGGTTTCAGAGATTCCTCGCCTCAG	3907		

Query Match	15.2%	Score 173;	DB 4;	Length 22484;
Best Local Similarity	68.3%;	Pred. No. 2.9e-39;		
Matches 250;	Conservative 0;	Mismatches 115;	Indels 1;	Gaps 1;
15086	TTGGGAAGACAGGAGGACAAGAACAGGCTCCACGAAGAGATTTTCAGAGCAGAGCTGCGGTAC	157		
15086	TGGGTTTCACAGGGGAACATAACCAAGCTCACTACAGATAGTCTTTTTTTTTTTTTTTTT	15145		
15146	TNNCTTTCTGACACGGAGTCTCGCTTTGTTCNCAAGGCTGGAGTGCAGTGGTGTGACT	15205		
218	CGGCTCACTCAGCGTTTGACCTCCACAGGCTCAAGTGATCTCTCGTCTCAGCTTTTCCAAG	277		
15206	CAGCTCACTGCAACCTCTGCTCCCTGGTTCAGGAATTTCTCCTGCCTCAGCCTCCAGAG	15265		
278	TAACTGGGACCACACAGGCGATGCATCCACACGTAGGCTATTGTTTTTACATTTTTTGTAGAG	337		
15266	TAGCTGGGATTTACAGGCACCTGCCATCATGCCCAAGCTAAAT-TTTTTGTATTTTTTAGTAGAG	15324		
338	ATGGGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCCCTGGGCTCAAGCAATCCGCTC	397		
15325	ACGGGGTTTACCAATGTTGCCCTAGGCTGGTCTCAAACTCCCGGGCTCAAGCGATCCACCC	15384		
398	ACGTCMAACCTCCCAAAATGCTGGGATTTACAGGCGGTGAGCCACCGGGCCAGGGCTGAGTAA	457		
15385	GCCTTGGCTTCCCAAAAGTCTGGGATTTACAGGCGGTGAGCCACCGGGCTGGCCAGAAATAA	15444		
458	TCCTAA 463			
15445	TCTTAA 15450			

RESULT 12

```

US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent NO. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODUL
; FILE REFERENCE: PFS-0207
; CURRENT APPLICATION NUMBER: US/09/7
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-798-096-10

```

	Query Match	15.2%;	Score 173;	DB 4;	Length 99500;
	Best Local Similarity	74.4%;	Fred. No. 6.6e-39;		
	Matches 218;	Conservative	0;	Mismatches. 75;	Indels 0; Gaps 0;
QY	161	TTTTTTCTTTTTCTTTTTCTGTGTCCACCCAGGCTCAAGTACAGTGGTTAGCTCACGG	220		
DB	35956	TTTTTTTTTGAGACAGTCTCGCTCTGTACCACGAGCTGGAGTGAAGTGTGTTATGTCATCTGG	36015		
QY	221	CTCACTGCAGCTTTGACCTCCACGAGCTCAAGTGATCCTCTCGTCTCAGCTTTTCCAAGTAA	280		
DB	36016	CTCACTGCAGCCTCCACCTCCCGGGTTCAAGTGTATCTTGTGCCTCAGCCTCCCAGGTAG	36075		
QY	281	CTGGGACCAACAGCATGCAATCACCAAGTGTAGGCTATTGTTTACATTTTTTGTAGAGATG	340		
DB	36076	CTGGAACTACAGGTGCACACCAACCATGCTCGGCTAAATTTTTGTATTTCTCAGTAGACAGC	36135		
QY	341	GGGTCTCACCATGTTGCCACAGTTGGTCTCAAACTCCTGGGCTCAAGCAATCCCGCTCACG	400		
DB	36136	AGCTTTTTCCTCTCTGCTTGTAGCTTGTGACCTCTTGAACCTCTGAGCTCAGGCAATCCGCGCCG	36195		

Tue Jun 10 08:56:18 2003

```

QY 209 GTTAGCTACGGCTCACTGCAGCTTTGACCTCCAGGCTCAAGTGATCCTCTCGTCTCAG 268
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3848 GAGCGATCTCGGCTCACTGCAACCTCCGCTCCTGGTTCAAGAGATTCTCTGCTCTCAG 3907
QY 269 CTTTCCAGTAAGTGGGACCAAGGATGATCACCAGCTAGGCTATTGTTTACATTT 328
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3908 CTTCCCAAGTAGTGGGATTACAGGTGCCACCAACGCTGGCTAGTTTTTGTATTT 3967
QY 329 TTTGTAGAGATGGGTTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGC 388
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
3968 TTAGTAAAGATGGGTTTCAACCATGTTGGCAGGCTGGTCTTGAACCTCTGACATCAGGT 4027
QY 389 AATCCGCTCAGTCAACCTCCCAATGCTGGGATTACAGGCTGAGCCACCGGCCAGG 448
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
4028 GATCCGCCACCTTAGCCTCCCAAGTGTGGGATTACAGGCTGAGCCACCATACCTGG 4087
QY 449 GCTGACTAATCCTAATACAGGATTTTAAAGAACTT 487
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
4088 CCAGCAAAACCTCTTTAACTTGTTCCATGGGCTCCTT 4126

```

Search completed: June 7, 2003, 22:26:35
Job time : 189 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	190.2	16.7	66804	10	US-09-740-041-3	Sequence 3, Appli
c	185.4	16.2	916	9	US-09-764-891-8218	Sequence 8218, Ap
2	183.4	16.1	735	9	US-09-764-891-8245	Sequence 8245, Ap
c	182	16.0	288	9	US-10-115-278-1	Sequence 1, Appli
3	181.4	15.9	174424	10	US-09-967-768A-314	Sequence 314, App
c	180	15.8	21470	9	US-10-092-154-1157	Sequence 1157, Ap
4	180	15.8	21470	10	US-09-764-847-1157	Sequence 1157, Ap
c	179.8	15.8	1423	9	US-09-796-753-97	Sequence 97, Appl
c	179.8	15.8	1423	9	US-09-796-753-111	Sequence 111, App
c	179.8	15.8	1440	12	US-10-067-422-6	Sequence 6, Appli
10	179	15.7	7233	9	US-10-091-504-2123	Sequence 2123, Ap
c	179	15.7	7233	10	US-09-764-869-2123	Sequence 2123, Ap
11	178.6	15.7	1125	9	US-10-091-438-77	Sequence 77, Appl
c	178.6	15.7	1125	10	US-09-764-853-209	Sequence 209, App
12	178.6	15.7	20190	9	US-09-996-015-3	Sequence 3, Appli
c	178.6	15.7	66804	10	US-09-740-041-3	Sequence 3, Appli
13	178.4	15.6	16181	9	US-10-092-154-1426	Sequence 1426, Ap
c	178.4	15.6	16181	9	US-09-764-891-6956	Sequence 6956, Ap
14	178.4	15.6	16181	10	US-09-764-847-1426	Sequence 1426, Ap
c	178.4	15.6	16181	10	US-09-764-891-6956	Sequence 6956, Ap

	Query Match	16.7%	Score 190.2	DB 10	Length 66804
	Best Local Similarity	70.2%	Pred. No. 1.1e-46		
	Matches 255	Conservative 0	Mismatches 108	Indels 0	Gaps 0
QY	86	ATGAGAGAGCTGTGGCAAGACAGACAGGACACAGAGCTCCACGACAGAGATTTCAGAGC	145		
DB	45572	ATTGAGGAGCTGGAATGAGACAGCAGGCCTCTTGCCATCTGGAATTTAATGTTCAACCC	45631		
QY	146	AGAGCTGCGTACTCTCTTTCTTTTGTCTCTCTGCTCTGACCCAGGCTGAAGTACA	205		
DB	45632	TCACCTTTTTTTTTTTTTTTTTTTTGATACAGTCACCTCTGTCACCCAGGCTGGATGCA	45691		
QY	206	GTGTTAGCTCACGGCTCAGTCAGCTTTGACTCCACAGGCTCAAGTGATCCTCTCGTCT	265		
DB	45692	GTGGTGAGATCTTGCTCAGTCGAACCTCCGCCTCAGGGTTCGAAGCAATTCCTCGTGCT	45751		
QY	266	CAGCTTTTCCAAGTAATCGGACACAGCATGATCACCAGCTGAGCTATTGTTTTACA	325		
DB	45752	CAGCGGCCAAGTAGCTGGGATTACAGCACGCGCCACCATGCCAGGCTAATTTTTGTGA	45811		
QY	326	TTTTTTGTAGAGATGGGGTCTCAGCATGTTGCCCAGGTTGGTCTCAAACTCCTGGGCTCA	385		


```
Db 94 CCAGGCTGGTCTGCAATCTCTGGGCTCAAGTGATCTCCCGCTCGGCTCCCAAAGTG 35
QY 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGCG 450
Db 34 CTGGGATTACAGCGCTGAGCCACCGGGCCCGGCC 1

RESULT 5
US-09-967-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 314
; LENGTH: 174424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-314

Query Match 15.9%; Score 181.4; DB 10; Length 174424;
Best Local Similarity 77.6%; Pred. No. 1e-43;
Matches 232; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 177 TTTTGTCTGTCAACCAGCTGAAGTACAGTGTAGCTCACGGCTCACTGCAAGCTTTGA 236
Db 154673 TCTGGCTGTCTCACTCAGGCTGGAGTGCAAGTGTGGTGCATCATGTGCTCACTGCAACCTCGA 154614

QY 237 CTTCCAGGCTCAAGTATCTCTGTCTCAGCTTCCAGTATCTGGGACACACAGGAT 296
Db 154613 CTTCCAGGTTCAAGTATCTCTCCCATCTCAGCTCCCGAGGCTGGGACTACAGATG 154554

QY 297 GCATCACCAAGCTAGGCTATTGTTTACATTTTGTAGATGGGCTCTCACCATTGTG 356
Db 154553 GTGCCACACGCGCGCTAATTTTTA-TTTTCTGTAGATGGGCTCTCATATGTTG 154495

QY 357 CCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAATG 416
Db 154494 CCAGGCTGGTCTCAAACTCTGACCTCAGGTGATCCACCTGCCTCGACCTCCCAAAGTG 154435

QY 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGCTGAGTAATCTTAATCAGGATTTT 475
Db 154434 CTGGGATTACAGCGCTGAGCCACCGGGCTGAAATGACCTTTTAAATAAATGTT 154376

RESULT 6
US-10-092-154-1157
; Sequence 1157, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1157
; LENGTH: 21470
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-092-154-1157

Query Match 15.8%; Score 180; DB 9; Length 21470;
Best Local Similarity 72.2%; Pred. No. 7.3e-44;
Matches 234; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 135 GATTTTCAGAGCAGAGCTGGTACTCTCTTTTCTTTTGTGTTTCTTTTGTCTCTGTCAACCCAG 194
Db 1585 GAGGTGACTGAAGAATTGAATTTTGTGTTTGTGAGACGGAGTCTTGCTCTGTCAACCCAG 1644

QY 195 GCTGAAGTACAGTGGTTAGCTCAGCGCTCAGTGCAGCTTTGACCTCCAGGGCTCAAGTGA 254
Db 1645 GCTGAGTGCAGTGGCGTGATCTTGCTCAGTGCATCTCCGCTCCAGGGCTCAAGCGA 1704

QY 255 TCCTCTCGTCTCAGCTTTTCCAAAGTAACCTGGGACCAACAGGATGATCACCAGCTAGGCT 314
Db 1705 TTCTCTCGCTCAGGCTCTCTGAGTAACCTGGGATTAAGTGCACACACAGCGCTGGCT 1764

QY 315 ATTGTTTACATTTTGTAGAGATGGGCTCTCAGCATGTTGCCAGGTTGGTCTCAAAAC 374
Db 1765 AATTTTGTATTTTGTAGTAGACAGGCTTTTCAAAATGTTGCCAGGCTGGTCTCAAAAC 1824

QY 375 TCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAAATGCTGGGATTAAGGCGTGA 434
Db 1825 TCCTGACCTCAAGTGTGCGCGCGCTCGGCTCCCAAAGTGTGGGATTAAGGCTGTA 1884

QY 435 GCCACGGGCGGCGCTGAGTAAT 458
Db 1885 GCCACTGTGCTGGCTGAAATAAT 1908

RESULT 7
US-09-764-847-1157
; Sequence 1157, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1157
; LENGTH: 21470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1157

Query Match 15.8%; Score 180; DB 10; Length 21470;
Best Local Similarity 72.2%; Pred. No. 7.3e-44;
Matches 234; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 135 GATTTTCAGAGCAGAGCTGGTACTCTCTTTTCTTTTGTGTTTCTTTTGTCTCTGTCAACCCAG 194
Db 1585 GAGGTGACTGAAGAATTGAATTTTGTGTTTGTGAGACGGAGTCTTGCTCTGTCAACCCAG 1644

QY 195 GCTGAAGTACAGTGGTTAGCTCAGCGCTCAGTGCAGCTTTGACCTCCAGGGCTCAAGTGA 254
Db 1645 GCTGAGTGCAGTGGCGTGATCTTGCTCAGTGCATCTCCGCTCCAGGGCTCAAGCGA 1704

QY 255 TCCTCTCGTCTCAGCTTTTCCAAAGTAACCTGGGACCAACAGGATGATCACCAGCTAGGCT 314
Db 1705 TTCTCTCGCTCAGGCTCTCTGAGTAACCTGGGATTAAGTGCACACACAGCGCTGGCT 1764

QY 315 ATTGTTTACATTTTGTAGAGATGGGCTCTCAGCATGTTGCCAGGTTGGTCTCAAAAC 374
Db 1765 AATTTTGTATTTTGTAGTAGACAGGCTTTTCAAAATGTTGCCAGGCTGGTCTCAAAAC 1824

QY 375 TCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAAATGCTGGGATTAAGGCGTGA 434
Db 1885 TCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAAATGCTGGGATTAAGGCGTGA 434
```

1825 TCTGACCTCAAGTGTCCGCCGCTCGGCTCCCAAGTCTCGGATTACAGGTGTA 1884

435 GCCACCGCGCCAGGGCTGAGTAAT 458
1885 GCCACTGTGCTGGCTGAATAT 1908

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(444)
US-09-796-753-97

Query Match 15.8%; Score 179.8; DB 9; Length 1423;
Best Local Similarity 76.7%; Pred. No. 1.5e-44;
Matches 220; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 177 TTTTGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGCTCAGCGCTCACTGCAGCTTTGA 236
DB 1385 TCTCACTCTGTCAACCCAGGCTGGAGTACGGTGTCAATGATCAGACTCAGTGCAGCTCTTA 1326
QY 237 CCTCCAGGCTCAAGTATCTCTCGTCTCAGCTTTTCCAAAGTAACTGGGACCAAGCAT 296
DB 1325 CCTCCAGGCTCAAGTATCTCTCACTTCAAGCTCCCTTTGTAGATGGGCTCTTGTCTATGTTG 1266
QY 297 GCATCACCACTAGGCTATTTTATCATTTTGTAGATGGGCTCTCACCATTGTTG 356
DB 1265 GTGCCACCACACTTGGCTAAATTTTAAATTTTGTAGATGGGCTCTTGTCTATGTTG 1206
QY 357 CCCAGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACTCAACCTCCCAAAATG 416
DB 1205 CCCAGGCTGGTCTCAAAATCTCTGGGCTCAAGTGCTTTTTCGCTCAGCTCCCAAAATG 1146
QY 417 CTGGATTACAGGCTGAGCCACCGGGCCAGGGCTGAGTAATCTCTAA 463
DB 1145 CTGGACTACAGACATGAGCTACTGCGCCAGGCTTAGAAAACTTA 1099

RESULT 9
US-09-796-753-111/c
Sequence 111, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 97
LENGTH: 1423
TYPE: DNA

US-09-796-753-97/c
Sequence 97, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 97
LENGTH: 1423
TYPE: DNA

; PRIOR FILING DATE: 1999-08-03
 ; PRIOR APPLICATION NUMBER: 60/131,672
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/130,693
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 1440
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-067-422-6

Qy	357	CCACGGTGTGTCTCAAAATCTCTGGGCTCAAGCAATCCGCTCAGTCAACTTCTCCCAAAATG	416
Db	1232	CCCAGGCTGGTCTCAAAATCTCTGGGCTCAAGTGTCTTTTCGGCTCAGCCTCCCAAAGTG	1173
Qy	417	CTGGGATTACAGGGGTGAGCCACGGGGCCAGGCTCAGTAACTCCTAA	453
Db	1172	CTGGGACTACAGACATGAGTACTTGGGGCCAGGCTTTAGAAACTTTTA	1126

RESULT 11
US-10-091-504-2123/c
; Sequence 2123, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

	Query Match	15.7%;	Score 179;	DB 9;	Length 7233;	
	Best Local Similarity	77.6%;	Pred. No. 7.4e-44;	Mismatches 65;	Indels 1; Gaps 1;	
	Matches 229;	Conservative 0;				
Qy	158	TCTTTTTCCTTTTTGTTTCTTTTGCTCTGTCA	CCCAGGCTGAAGTACAGTGGTTAGCTCA	217		
Dd	3492	TCTTTTCTTTTGAGAGAGGGTTTTATTCTGTCA	CCCAGGCTGGAGTGGCACCATCA	3433		
Qy	218	CGGCTCACTGCAGCTTGACTCCCAGGCTCAA	GTAATCCTCTCGTCTCAGCTTTTCCAAG	277		
Dd	3432	GGGCTCACTGCAGCTCGACTCTCTGGGCTCA	AGTATCTCTCTGCTCAGCCTCCCAAG	3373		
Qy	278	TAACTGGGACCA CAGGCATGCATCACACGTA	AGGCT -ATTGTTTTACATTTTTTGPAGA	336		
Dd	3372	TAGCTGGGACTACAGG CATATACACACACAC	CCTGGGCTAATTTTTTTGTA TTTTTTAGTTGA	3313		

RESULT 13
US-10-091-438-77/c
; Sequence 77, Application US/10091438
; Publication No. US20030077606A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT217C1
; CURRENT APPLICATION NUMBER: US/10/091,438
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,879
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11

7	PRIOR APPLICATION NUMBER: 50/249,297
7	PRIOR FILING DATE: 2000-11-17
7	PRIOR APPLICATION NUMBER: 50/232,400
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/231,242
7	PRIOR FILING DATE: 2000-09-08
7	PRIOR APPLICATION NUMBER: 50/232,081
7	PRIOR FILING DATE: 2000-09-08
7	PRIOR APPLICATION NUMBER: 50/232,080
7	PRIOR FILING DATE: 2000-09-08
7	PRIOR APPLICATION NUMBER: 50/231,414
7	PRIOR FILING DATE: 2000-09-08
7	PRIOR APPLICATION NUMBER: 50/231,244
7	PRIOR FILING DATE: 2000-09-08
7	PRIOR APPLICATION NUMBER: 50/233,064
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/233,063
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/232,397
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/232,399
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/232,401
7	PRIOR FILING DATE: 2000-09-14
7	PRIOR APPLICATION NUMBER: 50/241,808
7	PRIOR FILING DATE: 2000-10-20
7	PRIOR APPLICATION NUMBER: 50/241,826
7	PRIOR FILING DATE: 2000-10-20
7	PRIOR APPLICATION NUMBER: 50/241,786
7	PRIOR FILING DATE: 2000-10-20
7	PRIOR APPLICATION NUMBER: 50/241,221
7	PRIOR FILING DATE: 2000-10-20
7	PRIOR APPLICATION NUMBER: 50/246,475
7	PRIOR FILING DATE: 2000-11-08
7	PRIOR APPLICATION NUMBER: 50/231,243
7	PRIOR FILING DATE: 2000-09-08

155 TACTCCTTTTCTTTTGTGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGC 214

RESULT 14

```

US-09-764-853-209/c
; Sequence 209, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, P
; FILE REFERENCE: FUZ06
; CURRENT APPLICATION NUMBER: US/09/764
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - con

```

Tue Jun 10 08:56:18 2003

```

; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-853-209

Query Match      15.7%; Score 178.6; DB 10; Length 1125;
Best Local Similarity 75.1%; Pred.No.3e-44;
Matches 223; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY      155  TACTCCCTTTTCTTTTGTTCCTGCTGCTGACCCAGGCTGAAGTACAGTGTGTTAGC 214
DB      993  TATTGTGTTATCTGAGACAGGCTTCCTCTGTGACCCAGGCTGGAGTGCAGTGCACAA 934

QY      215  TCACGGCTCACTGCAGCTTTGACCTCCAGGCTCAAGTGATCCTCTCGCTCAGGTTTCC 274
DB      933  TCTCGACTCAATGCAACCTCCACCTCGGGGCTCAAGCGATCCTCTGTCTCAGCTTCCC 874

QY      275  AAGTAACCTGGAGCACACAGGCATGCATACACACGCTAGGCTATGTGTTTACATTTTTCGA 334
DB      873  AAGTAGCTGGGATCACAGGCATACACACACACCCCTGCTAAATTTTGTGTTATTTTTCGA 814

QY      335  GAGATGGGGTCTCACCATGTTGCCAGGTGGTCTCAAACTCCTCGGGCTCAAAGCAATCCG 394
DB      813  GAGATGAGGTCTGACCATGTTGCCAGGCTGCTCTAAACTCTGGACTCAAGTATCCA 754

QY      395  CTCAGCTCAACCTCCCCAAATGCTGGGATTACAGGGCTGAGCCACCGGGCCAGGGCT 451
DB      753  CTTGCTTTGGCTCTCCAAAGTCTGGATTGCAAGTGAAGCCACCGCACCCGGGCT 697

```

```

RESULT 15
US-09-996-015-3
; Sequence 3, Application US/09996015
; Publication NO. US2003032166A1
GENERAL INFORMATION:
; APPLICANT: Quinn, Kerry E.
; APPLICANT: Pena, Carol A. E.
; APPLICANT: Li, Li
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Leite, Mario W.
; TITLE OF INVENTION: Aortic Carboxypeptidase-Like Proteins and Nucleic Acids
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 15966-581 CIP
; CURRENT APPLICATION NUMBER: US/09/996,015
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 09/641,741
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/159,613
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: 60/175,534
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/224,086
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 20190
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2206)
; OTHER INFORMATION: Wherein n is A, C, G, or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2207)
; OTHER INFORMATION: Wherein n is A, C, G, or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2209)

```


Db 3818 CTGGATTACAGCGGTGAGCCACCGCGCGCGCCAGTTAAA 3858

Search completed: June 7, 2003, 23:24:23
Job time : 281 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 20:36:07 ; Search time 1597 Seconds
(without alignments)
11571.102 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagcagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gas:*

18: em_gas_hum:*

19: em_gas_inv:*

20: em_gas_pln:*

21: em_gas_vrt:*

22: em_gas_fun:*

23: em_gas_nam:*

24: em_gas_mus:*

25: em_gas_other:*

26: em_gas_pro:*

27: em_gas_rod:*

Result No.	Score	Query Match	Length	ID	Description
C 1	197.8	17.3	496	17 B35967	B35967 HS-1031-A2-
C 2	195	17.1	568	9 AUI59406	AUI59406 AUI59406
C 3	186.2	16.3	410	9 AIO23375	AIO23375 ow63g02.x
C 4	186	16.3	515	14 BM679408	BM679408 UI-E-E00-
C 5	184.2	16.1	708	17 AGI43040	AGI43040 Pan trogl
C 6	184.2	16.1	713	17 AQ312217	AQ312217 RPC111-10

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	183.6	16.1	655	17	AG169306
8	183	16.0	643	9	AI114719
9	183	16.0	2167	11	AF116633
10	182.4	16.0	390	14	R56162
11	182.4	16.0	742	17	AQ343483
12	181.8	15.9	649	17	BH609847
13	181.6	15.9	524	10	AW973992
14	180.6	15.8	571	9	AA131088
15	179.8	15.8	331	12	BG057233
16	179.8	15.8	661	10	BE177530
17	179.8	15.8	698	17	AG141964
18	179.6	15.7	430	17	AQ393433
19	179.4	15.7	424	9	AI499954
20	179.2	15.7	373	9	AL596605
21	179.2	15.7	531	14	BQ270554
22	179.2	15.7	559	12	BG537830
23	179.2	15.7	713	12	BG684208
24	179.2	15.7	893	13	BI913559
25	178.8	15.7	785	14	BM721013
26	178.8	15.7	1048	9	AL576528
27	178.8	15.7	2205	11	AF318346
28	178	15.6	455	17	AQ392348
29	178	15.6	558	17	AQ527359
30	177.8	15.6	379	10	AV754799
31	177.8	15.6	684	17	AG037064
32	177.6	15.6	430	14	BQ277407
33	177.6	15.6	617	14	BQ181121
34	177.4	15.5	456	9	AI753334
35	177.4	15.5	512	17	AQ538435
36	177.2	15.5	416	17	AQ748789
37	177.2	15.5	515	17	AQ506282
38	177	15.5	532	17	AQ701252
39	177	15.5	632	9	AI821267
40	176.6	15.5	562	17	AQ778690
41	176.6	15.5	701	17	AG148726
42	176.4	15.5	512	17	AQ120174
43	176.4	15.5	604	14	BM990713
44	176.4	15.5	950	17	AQ749313
45	176.2	15.4	471	10	AW151925

ALIGNMENTS

RESULT 1
B35967/c

LOCUS
HS-1031-A2-F07-MR-V0001.abi

DEFINITION
sapiens genomic clone Plate=CT 811 Col=14 Row=K, DNA sequence.

ACCESSION
B35967

VERSION
B35967.1

KEYWORDS
GSS

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 496)

AUTHORS
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.

TITLE
Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

JOURNAL
Unpublished (1997)

COMMENT
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: K column: 14
Class: BAC ends
High quality sequence stop: 496.

B35967 496 bp DNA linear GSS 17-OCT-1997
HS-1031-A2-F07-MR-V0001.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 811 Col=14 Row=K, DNA sequence.

B35967
sapiens genomic clone Plate=CT 811 Col=14 Row=K, DNA sequence.

B35967.1 GI:2535336

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 496)

Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.

Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

Unpublished (1997)

Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: K column: 14
Class: BAC ends
High quality sequence stop: 496.

AG169306 Pan trogl
AI114719 HAI318 Hu
AF116633 Homo sapi
R56162 Y91b06.r1
AQ343483 RPC111-12
BH609847 HVI13C04
AW973992 EST385990
AA131088 zol6c04.8
BG057233 7f75d01.x
BE177530 RCI-H0509
AG141964 Pan trogl
AQ393433 CITBI-E1-
AI499954 t063c10.x
AL596605 DRF29451C
BQ270554 ik05a03.x
BG537830 602566186
BG684208 602635838
BI913559 603180311
BM721013 UI-E-E00-
AL576528 AL576528
AF318346 Homo sapi
AQ392348 CITBI-E1-
AQ527359 RPCI-11-3
AV754799 AV754799
AG037064 Pan trogl
BQ277407 AGENCOURT
BQ181121 UI-H-EUO-
AI753334 cr08f09.x
AQ538435 RPCI-11-3
AQ748789 HS-5574_A
AQ506282 RPCI-11-3
AQ701252 HS-2132_A
AI821267 ab9f0f07.x
AQ778690 HS-2235_A
AG148726 Pan trogl
AQ120174 HS-3028_B
BM990713 UI-H-D10-
AQ749313 HS-5576_A
AW151925 xf70d02.x

FEATURES
 source
 Location/Qualifiers
 1. .496
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="PlateCT 811 Col=14 Row=K"
 /clone_lib="CIT Human Genomic Sperm Library C"
 /sex="M"
 /notes="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"
 BASE COUNT 155 a 85 c 135 g 120 t 1 others
 ORIGIN
 Query Match 17.3%; Score 197.8; DB 17; Length 496;
 Best Local Similarity 70.3%; Pred. No. 2.5e-29;
 Matches 265; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
 QY 161 TTTTCTTTTGTGTTCTTTGCTCTGTCACCCAGGCTGAAGTACAGTGTAGCTCACGG 220
 Db 487 TCTCTCTTTTTCACGGGGTGTGCTCTGTCTACCCAGGCTGGAGTACAGTGTATGATCACAG 428
 QY 221 CTCACCTGCAGCTTTGACCTCCAGGCTCAAGTACCTCTCTGCTCAGCTTTTCCAAGTAA 280
 Db 427 CTCACCTGCAGCTTTGACCTCCAGGCTCAAGTACCTCTCTGCTCAGCTTTTCCAAGTAA 368
 QY 281 CTGGGACCAAGCATGTCATCACACGCTAGGCTATTTGTTTACATTTTGTAGAGATG 340
 Db 367 CTGGGACCAAGCATGTCATCACACGCTAGGCTATTTGTTTACATTTTGTAGAGATG 308
 QY 341 GGGTCTCACATGTTGGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACG 400
 Db 307 GAGTCTCACATTTGTTGCCAGGCTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACG 248
 QY 401 TCAACCTCCCAATGCTGGGATACAGGCTGAGCCACCGGCGCCAGGCTGAGTAATCC 460
 Db 247 TCAGATCCCAAGTGTGGGATACAGGCTGAGCCACCGGCGCCAGGCTGAGTAATCC 188
 QY 461 TAATCAGAGATTTTAAAGAAACTTCTCGCCACCCATTAACAAATATCTCTCTACCA 520
 Db 187 CAATATTAGTTTCTCCACCTCCATTCAACAAACACCATCATGCTCATATCTTGATA 128
 QY 521 ATTGGTAGTAATATT 537
 Db 127 AATGAGAATTTATTAATT 111
RESULT 2
 AU159406 568 bp mRNA linear EST 05-AUG-2002
 LOCUS
 DEFINITION
 AU159406 THYRO1 Homo sapiens cDNA clone THYRO1001595 3', mRNA sequence.
 ACCESSION
 AU159406
 VERSION
 AU159406.1 GI:11020927
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, Y., and Isogai, T.).
 TITLE
 HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano, S., Isogai, T.).
 JOURNAL
 COMMENT
 Unpublished (2000)
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
FEATURES
 source
 Location/Qualifiers
 1. .568
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="THYRO1001595"
 /clone_lib="THYRO1"
 /tissue_type="thyroid gland"
 /note="Vector: pME18SFL3"
 BASE COUNT 141 a 148 c 128 g 142 t 9 others
 ORIGIN
 Query Match 17.1%; Score 195; DB 9; Length 568;
 Best Local Similarity 80.6%; Pred. No. 8.5e-29;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 177 TTTTGTCTGTCTCACCAGGCTGAAGTACAGTGTAGCTCAGGGCTCACTGACGCTTTTGA 236
 Db 13 TCTTGTCTGTCTCACCAGGCTGAAGTGTGAGTGGCAGCATCACTGCTCACTGACGCTTTGA 72
 QY 237 CTCTCCAGGCTCAAGTATCTCTCTGCTCTCAGCTTTTCCAAAGTAACTGGGACACACAGCAT 296
 Db 73 CTCTCCAGGCTCAGGTGATCTCTCCACCTCCAGCTCCCGAGTAGCTGGGACTACAGGCAT 132
 QY 297 GCATCACCACGCTAGGCTATTTTACATTTTGTAGAGATGGGCTCTCACCAGTTG 356
 Db 133 GCACACACGCTCAGCTCAAGTAAATTTTGTACTTTTGTAGACGGGTTTCACTAGTTG 192
 QY 357 CCCAGGTGCTCTCAAACTCTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAAAATG 416
 Db 193 CACAGGCTGCTCTCAGCTCTCTGGGCTCAAGCTATCCGCTGCTCGGCTCCCAAGTG 252
 QY 417 CTGGGATTAACAGCGGTGAGCCACCGGCGCCAGGCTGAGTAATC 459
 Db 253 CTGGGATTAACAGCGGTGAGCCACCGGCGCCAGGCTGAGTAATC 295
RESULT 3
 AU1023375/c 410 bp mRNA linear EST 28-AUG-1998
 LOCUS
 DEFINITION
 AU1023375.1 GI:3239781
 AU1023375
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL
 COMMENT
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1166 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 335.
FEATURES
 source
 Location/Qualifiers
 1. .410
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1651538"
 /clone_lib="Soares_senescent_fibroblasts_NbHSF"
 /tissue_type="senescent_fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V-TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTATCAATCTCAAGTGGAGCGCGCAATTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
Soares and M.Fatima Bonaldo."
BASE COUNT 126 a 85 c 112 g 87 t
ORIGIN

Query Match 16.3%; Score 186.2; DB 9; Length 410;
Best Local Similarity 70.7%; Pred. No. 5.1e-27;
Matches 248; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 142 GAGCAGAGCTGGTACTCTCTTTCTTTTGTCTCTCTGTCACCGAGGTGAG 201
Db GAGCAGAGCTGGTACTCTCTTTCTTTTGTCTCTCTGTCACCGAGGTGAG 201
QY 409 GGGCTGGCTCATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 350
Db GGGCTGGCTCATTTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 350
QY 202 TACAGTGGTGTAGCTCAGGCTCACTGACGCTTGTACCTCCAGGCTCAAGTATCTCTC 261
Db TACAGTGGTGTAGCTCAGGCTCACTGACGCTTGTACCTCCAGGCTCAAGTATCTCTC 261
QY 349 TCGAGTGGTATGATCTGGCTCACTGACCTCCAGCTCCAGGCTCAAGGATCTCTCC 290
Db TCGAGTGGTATGATCTGGCTCACTGACCTCCAGCTCCAGGCTCAAGGATCTCTCC 290
QY 262 GTCTCAGCTTTTCAAGTAACTGGGACACAGGCGATCATCACCAGCTAGGCTATTGTTT 321
Db GTCTCAGCTTTTCAAGTAACTGGGACACAGGCGATCATCACCAGCTAGGCTATTGTTT 321
QY 289 AACTCAGCTCCCAAGTAGCTGGACTACAGGTACATGCCACACACACCTGGCTGATTTTC 230
Db AACTCAGCTCCCAAGTAGCTGGACTACAGGTACATGCCACACACACCTGGCTGATTTTC 230
QY 322 TACATTTTTGTAGAGATGGGTCTCAGCATGTGGCCAGGTTGGTCTCAAACTCTGGG 381
Db TACATTTTTGTAGAGATGGGTCTCAGCATGTGGCCAGGTTGGTCTCAAACTCTGGG 381
QY 229 TGTATTTTTAGTAGAGTGGGTTTCCACCATGTGGCCAGGCTGCTTGAACCTCTGAG 170
Db TGTATTTTTAGTAGAGTGGGTTTCCACCATGTGGCCAGGCTGCTTGAACCTCTGAG 170
QY 382 CTCAAGCAATCCGCTCACGCTCAACCTCCCAATGCTGGGATTACAGGCGTGACGACCG 441
Db CTCAAGCAATCCGCTCACGCTCAACCTCCCAATGCTGGGATTACAGGCGTGACGACCG 441
QY 169 CTCAGTGATCACTGCTTGGCTCCGAGTGTCTGGATTACAGGCTGAGGCCACCA 110
Db CTCAGTGATCACTGCTTGGCTCCGAGTGTCTGGATTACAGGCTGAGGCCACCA 110
QY 442 GGCAGGCGTGAGTAACTCAATCAGGATTTTAAAGAAAGAACTTCCTGC 492
Db GGCAGGCGTGAGTAACTCAATCAGGATTTTAAAGAAAGAACTTCCTGC 492
QY 109 TGCCAGCGCAATGATTCATTTTCAACTGCTGCTCTGTGTAGTGACTTC 59
Db TGCCAGCGCAATGATTCATTTTCAACTGCTGCTCTGTGTAGTGACTTC 59

RESULT 4
BM679408
LOCUS
DEFINITION
UI-E-E00-ahz-1-04-0-UI.s1 UI-E-E00 Homo sapiens cDNA clone
UI-E-E00-ahz-1-04-0-UI 3', mRNA sequence.
BM679408
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA
sequence: 12-302, >ALU (matched complement)
Seq primer: M13 Forward
POLVA=Yes.

FEATURES

source
Location/Qualifiers
1..515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-E00-ahz-1-04-0-UI"
/clone_lib="UI-E-E00"
/tissue_type="fetal eye"
/dev_stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-E00 is a cDNA library containing the following
tissue(s): fetal eye. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGGTATACC. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_L1B=UI-E-E00
TAG_TISSUE=human fetal eye
TAG_SEQ=CCGGTATACC"

BASE COUNT 130 a 126 c 100 g 157 t 2 others
ORIGIN

Query Match 16.3%; Score 186; DB 14; Length 515;
Best Local Similarity 79.9%; Pred. No. 5.3e-27;
Matches 219; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 180 TGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGTCTCAGGCTCACTGAGCTTTGACCT 239
Db TGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGTCTCAGGCTCACTGAGCTTTGACCT 239
QY 240 CCCAGGCTCAAGTATGATCTCTCTGCTCAGCTTTTCAAGTAACTGGGACACAGGATGCA 299
Db CCCAGGCTCAAGTATGATCTCTCTGCTCAGCTTTTCAAGTAACTGGGACACAGGATGCA 299
QY 92 CCAGGCTCAGGGATCTTACCCAGCTCAGCTTCCAGGTAGTGGAGCCACAGGATGG 151
Db CCAGGCTCAGGGATCTTACCCAGCTCAGCTTCCAGGTAGTGGAGCCACAGGATGG 151
QY 300 TCACACAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCACCATGTTGCC 359
Db TCACACAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCACCATGTTGCC 359
QY 152 CCACCATGCTGGCTAATTTTTCGTATTTTGTAGAGACAGGGTTTTCCTCATGTTGCC 211
Db CCACCATGCTGGCTAATTTTTCGTATTTTGTAGAGACAGGGTTTTCCTCATGTTGCC 211
QY 360 AGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAAAATGCTG 419
Db AGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAAAATGCTG 419
QY 212 AGGCTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAGCTCCCAAAATGCTG 271
Db AGGCTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAGCTCCCAAAATGCTG 271
QY 420 GGATTACAGGCGTGAGCCACCGGGCCAGGCTGA 453
Db GGATTACAGGCGTGAGCCACCGGGCCAGGCTGA 453

RESULT 5

AG143040/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-003J20.TJ, genomic survey
sequence.
AG143040
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphocytes DNA, clone: RP43-003J20.TJ.
Male BAC Library clone: RP43-003J20.TJ.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1

Email: est@watson.wustl.edu

Insert Size: 1266

High quality sequence stops: 349 Source: IMAGE Consortium, LNLNL
This clone is available royalty-free through LNLNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

Insert Length: 1266 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 349.

Location/Qualifiers

1. .390

/organism="Homo sapiens"

/db_xref="GDB:413317"

/db_xref="taxon:9606"

/clone="IMAGE:40776"

/clone_lib="Soares infant brain LNIB"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not I; Site 2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lfamid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 80 a 107 c 84 g 117 t 2 others

ORIGIN

Query Match 16.0%; Score 182.4; DB 14; Length 390;

Best Local Similarity 69.7%; Pred. No. 2.9e-26;

Matches 246; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

Qy 140 CAGACGAGCTGGGACTCCTTTTCTTTTGTGTTTCTGTCTGTCTCACCAGGCTGA 199

Db 1 CCGCGCTGGCCCTCATTTTGTGTTTGTGAGACATCTTACTCTGTCAACCAGGCTGG 60

Qy 200 AGTACAGTGTGTAGCTCACGGCTCAGTCGAGCTTTGACCTCCAGGCTCAAGTGAATCCTC 259

Db 61 AGTGCAGTGTATGATCTCGGCTCACTGCAACCTCCAGCTCCAGGCTCAAGGATCCTC 120

Qy 260 TCGTCTCAGTTTCCAAAGTAACCTGGGACACAGGCATGATCACACGCTAGGCTATTGT 319

Db 121 CCAACTCAGCTCCCAAGTAGTGGGACTACAGGTACATGCACACACACTGGCTGATTT 180

Qy 320 TTTACATTTTGTAGAGATGGGCTTCACCATGTGCGCAGTTGGTCTCAAACTCCTG 379

Db 181 TCTGTATTTTGTAGTAGAGTGGGCTTTCACCATGTGCGCAGGCTGGTCTTGAACCTCTG 240

Qy 380 GGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATGTGGGATTACAGGGCTGAGCCAC 439

Db 241 AGCTCAAGTATCCACCTGCTTGGCTCCCGAGTGTGGGATTACAGGCTGACANCC 300

Qy 440 CGGCGCAGGCTGAGTAATCTTAATACAGGATTTTAAAGAAATCTCTGCG 492

Db 301 ATGGCCAGCGCAATGATTCATTTTCAACTGCTCTGTGTAGTGACTTTC 353

RESULT 11

AQ343483

LOCUS

DEFINITION RPCI11-122M10.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-122M10.DNA 742 bp linear GSS 07-MAY-1999

ACCSSION AQ343483

VERSION AQ343483.1 GI:4168379

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Zhao S, Adams M D, Nierman W, Malek J, de Jong P, and Venter

J.C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 Unpublished (1997)
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES

Location/Qualifiers

1. .742
 /organism="Homo sapiens"
 /db_xref="GDB:7546761"
 /db_xref="taxon:9606"
 /clone="RPCI-11-122M10"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 231 a 141 c 146 g 224 t

Query Match 16.0%; Score 182.4; DB 17; Length 742;
 Best Local Similarity 75.0%; Pred. No. 2.5e-26;
 Matches 228; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 161 TTTTCTTTTGTGTTCTGTGTCACCCAGGCTGAAGTACAGTGGTTAGCTCACGG 220
 |||||
 DB 231 TTTTGTGATACAGGGTTTCACTCTGTCAACCAGGCTGGAGTACAGTAGTGAACATGG 230
 QY 221 CTCACGTGACGCTTGTACCTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAAAGTAA 280
 |||||
 DB 291 CTGACTGCAGCTTGTACCTCTGTGACTCAGTGTATCTCCGCTCAGCCTCCAAAGTAG 350
 QY 281 CTGGGACCAAGCATGTCATCACAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
 |||||
 DB 351 CTGGGACTACAGTGTGACCAACACCTTGTCTAAATTTTGTATTTTTGTAGAGACG 410
 QY 341 GGCTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACG 400
 |||||
 DB 411 GGTTTGTGCATGTTGCCAGGCTGGTTTCAAAATTCCTGGCTCAAGCAATCCTCTGTC 470
 QY 401 TCACCTCCCAAAATGCTGGGATACAGGCTGAGCCACCGGCGGCTGAGTAAATCC 460
 |||||
 DB 471 TTGGCTCCCTTAAGTTCTGAGATACAAAGTGTGAGCCACGCTGCTGGCTGTTGTATA 530
 QY 461 TAAT 464
 |||||
 DB 531 TACT 534

RESULT 12

BH609847/c
 LOCUS 649 bp DNA linear GSS 18-DEC-2001
 DEFINITION HIV13C04 SupT1 HIV-I in vivo integration lines Homo sapiens genomic
 Clone HIV13C04, DNA sequence.
 ACCESSION BH609847
 VERSION BH609847.1 GI:17922456
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 649)
 Schroder,A.R.W., Shinn,P., Chen,H., Berry, C., Ecker,J.R. and
 Bushman,P.
 Favored Sites for HIV-1 Integration in the Human Genome
 Unpublished (2002)
 Contact: Frederic Bushman
 Salk Institute Infectious Disease Laboratory
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1630
 Fax: 858 554 0341
 Email: bushman@salk.edu
 Class: PCR with specific primers.
 Location/Qualifiers

FEATURES

source

1. .649
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HIV13C04"
 /cell_line="SupT1"
 /note="A human T-cell line (SupT1) was infected with an
 HIV-based vector. DNA was isolated and cleaved with
 restriction enzymes; linkers were ligated onto the cleaved
 DNA and DNAs were amplified using one primer that bound to
 the linker DNA and one that bound to the HIV cDNA.
 Junctions between integrated HIV proviruses and cellular
 DNA were cloned and sequenced."
 BASE COUNT 228 a 88 c 170 g 163 t

Query Match 15.9%; Score 181.8; DB 17; Length 649;
 Best Local Similarity .77.9%; Pred. No. 3.4e-26;
 Matches 219; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 161 TTTTCTTTTGTGTTCTGTGTCACCCAGGCTGAAGTACAGTGGTTAGCTCACGG 220
 |||||
 DB 305 TTTTCTTTTGTGTTCTGTGTCACCCAGGCTGCAGTGCAGTGGCGGATCTCAG 246
 QY 221 CTCACGTGACGCTTGTACCTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAAAGTAA 280
 |||||
 DB 245 CTCACGTCAACCTTCAACCTCCAGGTTCAAGTATCTCTGCTCAGCTCCCAAGTAG 186
 QY 281 CTGGGACCAAGCATGTCATCACAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
 |||||
 DB 185 CTGGGACTACAGGCACACACACGCTGCTAATTTTGTATTTTTGTAGAGACA 126
 QY 341 GGCTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACG 400
 |||||
 DB 125 GGCTTTTCAACATGTTGCCAGTCTGCTCTCAAACTCTAACTCAGGTGATCTGCCACC 66
 QY 401 TCACCTCCCAAAATGCTGGGATACAGGCTGAGCCACCG 441
 |||||
 DB 65 TCAGCTCCCAAGTCTAGGATTACAGGTGTAGGCCACCG 25

RESULT 13

AW973992
 LOCUS 524 bp mRNA linear EST 02-JUN-2000
 DEFINITION EST385990 MAGE resequencences, MAGM Homo sapiens cDNA, mRNA sequence.
 AW973992
 ACCESSION AW973992.1 GI:8165076
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 524)
 REFERENCE
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaepard,R., Gay,C., Holt
 I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 312.
Location/Qualifiers

FEATURES
source

1. .331
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3302809"
/clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
/tissue type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Sal1; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
BASE COUNT 78 a 88 c 73 g 92 t
ORIGIN

Query Match 15.8%; Score 179.8; DB 12; Length 331;
Best Local Similarity 76.7%; Pred. No. 1e-25;
Matches 220; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 177 TTTTGTCTGTCAACCCAGGCTGAAGTACAGTGTGTTAGTCAAGGCTCAGTGCAGCTTTGA 236
DB 12 TCTCACTCTGTCAACCCAGGCTGAGTACGGTGTATGATCAGAGCTCACTGCAGCCTCTA 71
QY 237 CCTCCAGGCTCAAGTGTACCTCTCGTCTCAGCTTTTCCAGTAACTGGGACCAACAGGCAT 296
DB 72 CCTTCCAGGCTCAAGTGTACCTCTCACTTCAAGGCTCCCTTGTAGCTGGGACCAACAGGTGC 131
QY 297 GCATCACACGCTAGGCTATTGTTTACATTTTGTAGAGATGGGTCTCACCATGTTG 356
DB 132 GTGCCACACACACTTGGCTAAATTTTAAATTTTGTAGAGATGGGTCTTGTATGTTG 191
QY 357 CCCAGTTGGTCTCAAACTCCTGGGCTCAAGCAATCGGCTCAGCTCAAGCTCCCAAAATG 416
DB 192 CCCAGGCTGTCTCAAAATCTCGGGCTCAAGTGTCTTTCGGCTCAGGCTCCCAAAATG 251
QY 417 CTGGGATTACAGGCTGAGCCACCGGCGGCGGCTGAGTAATCCTAA 463
DB 252 CTGGGACTACAGACATGAGCTACTGCGCCCGAGCCTTAGAAAACTTTA 298

Search completed: June 7, 2003, 22:23:20
Job time : 1604 secs

THIS PAGE BLANK (USPTO)